

SEQUENCE LISTING

<110> Institut Pasteur

<110> Bayer CropScience SA

<120> Mutagenesis of *Aspergillus* fungi and genes essential for growth

<130> D20128

<150> US 60/363 543

<151> 2002-03-13

<150> US 60/434 407

<151> 2002-12-19

<160> 199

<170> PatentIn Ver. 3.2

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<212> DNA

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<213> *Aspergillus fumigatus*

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<213> *Aspergillus fumigatus*

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Ile Thr Glu Arg Glu Ala Lys Tyr Met Ile Asp Gln Phe Leu Met Gly
      115             120             125

```

```

Pro His Gly Leu Arg Ala Gly Gly Lys His Gly Asn Gly Phe Thr Trp
      130             135             140

```

```

Val Val Asp Thr Asn Val Met Arg Glu Ala Val Leu Ala Leu Thr Ala
      145             150             155             160

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Asp Glu Val Thr Ser Ser Leu Leu Ser Thr Gly Ser Gly Ser Leu Pro
          165             170             175

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Lys Ser Pro Ile Leu Ser Ser Ala Cys Pro Gly Trp Ile Cys Tyr Ala
 180 185 190
 Glu Lys Thr His Pro Phe Ile Leu Pro His Leu Ser Arg Leu Lys Ser
 195 200 205
 Pro Gln Ala Leu Ser Gly Thr Phe Leu Lys Ser Val Leu Ser Lys Ala
 210 215 220
 Leu Gly Val Pro Pro Ser Gln Ile Trp His Leu Ala Ile Met Pro Cys
 225 230 235 240
 Phe Asp Lys Lys Leu Glu Ala Ser Arg Glu Glu Leu Thr Asp Ile Ala
 245 250 255
 Trp Ala Ser Thr Phe Thr Gln Ser Gln Thr Thr Pro Val Arg Asp Val
 260 265 270
 Asp Cys Val Ile Thr Thr Arg Glu Leu Leu Thr Leu Ala Thr Ala Arg
 275 280 285
 Gly Leu Ser Leu Pro Asn Leu Pro Leu Lys Pro Leu Pro Ala Ser Cys
 290 295 300
 Leu Thr Pro Phe Pro Asp Gln Ala Leu Glu Ser Phe Leu Phe Ser Lys
 305 310 315 320
 Ser Ser Ser Gly Gln Thr Val Glu Ser Gly Thr Ser Gly Gly Tyr Leu
 325 330 335
 His His Val Leu Gln Ile Phe Gln Ala Arg Asn Pro Gly Ser Lys Ile
 340 345 350
 Val Thr Gln Arg Gly Arg Asn Ala Asp Val Val Glu Tyr Val Leu Met
 355 360 365
 Ser Ser Gly Asp Glu Pro Leu Phe Arg Ala Ala Arg Tyr Tyr Gly Phe
 370 375 380
 Arg Asn Ile Gln Asn Leu Val Arg Lys Leu Lys Pro Ala Arg Val Ser
 385 390 395 400
 Arg Leu Pro Gly Ala Lys Pro Gln Ala Val Ser Ser Ser Ala Asn Arg
 405 410 415
 Arg Gln Pro Met Ser Arg Asn Ala Ala Pro Ala Gly Thr Gly Ala Asp
 420 425 430
 Tyr Ala Tyr Val Glu Val Met Ala Cys Pro Gly Gly Cys Thr Asn Gly
 435 440 445
 Gly Gly Gln Ile Arg Ile Glu Asp Ala Arg Glu Ala Val Pro Asn Ala
 450 455 460
 Leu Lys Glu Thr Ser Thr Glu Thr Pro Val Ala Ala Pro Lys Pro Thr
 465 470 475 480
 Pro His Glu Gln Arg Ala Trp Leu Ala Arg Val Asp Glu Ala Tyr Tyr
 485 490 495
 Ser Ala Asp Ser Asp Ser Glu Gly Ser Val Thr Thr Glu Pro Val Ser

500

505

510

Val Leu Ser Arg Asp Asn Gln Ile His Glu Phe Leu Asn Tyr Trp Ser
 515 520 525

Glu Lys
 530

<210> 7

<211> 942

<212> DNA

<213> *Aspergillus fumigatus*

<400> 7

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tccgtgtctc gtacgtctaa ccccttgcca accctcattg actatgcctg cgaattgttt 240
cttttggtgg aattgcgctg aacgggtgtt gttatattta gataccactc gagctccccg 300
tccccgggaa gaaaatggac gtgagtatta cttcacaact aaagaagatt tcctggatct 360
tgtgagcaag aatgccttta tcgagcatgc gcagtttggt ggcaattact acgggtactac 420
tgtgcaggca gtgaaggatg ttgcgcagaa gggcaagatc tgcgttctcg acattgagat 480
gaggtaataa tagtcctgca acgtgaactg atatgaccgg agaagcagag gaaatccatc 540
atcaaattgga ttgtagttca acccaaacaa cagctgacga ctgaattgca atagggcgtg 600
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gaagaactag agaaaagact gcgtgggaga gcaaccgaga ctgaggagag cttgacggta 720
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<210> 8

<211> 600

<212> DNA

<213> *Aspergillus fumigatus*

<400> 8

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aagatctgcy ttctcgacat tgagatgagg ggcgtgaaac aagtcaagcg caccgatctt 360
gatgctcgat tcttattttt agcaccctcg tcccttgaaag aactagagaa aagactgcgt 420
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ttggaatatg cggcgcagcc tggctctcat gataagattg tcgtgaacga tgacctggag 540
aaggcttata aggaactgcg ggattggatt gtcgacggtg gtaacttttg agcgcgtcaa 600

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<210> 9

<211> 200

<212> PRT

<213> *Aspergillus fumigatus*

<400> 9

Met Thr Thr Gly Ala Val Gln Arg Phe Arg Pro Val Val Val Ser Gly
 1 5 10 15

Pro Ser Gly Thr Gly Lys Ser Thr Leu Leu Lys Arg Leu Phe Ala Glu
 20 25 30
 Tyr Pro Asp Thr Phe Asp Leu Ser Val Ser His Thr Thr Arg Ala Pro
 35 40 45
 Arg Pro Gly Glu Glu Asn Gly Arg Glu Tyr Tyr Phe Thr Thr Lys Glu
 50 55 60
 Asp Phe Leu Asp Leu Val Ser Lys Asn Ala Phe Ile Glu His Ala Gln
 65 70 75 80
 Phe Gly Gly Asn Tyr Tyr Gly Thr Thr Val Gln Ala Val Lys Asp Val
 85 90 95
 Ala Gln Lys Gly Lys Ile Cys Val Leu Asp Ile Glu Met Arg Gly Val
 100 105 110
 Lys Gln Val Lys Arg Thr Asp Leu Asp Ala Arg Phe Leu Phe Leu Ala
 115 120 125
 Pro Pro Ser Leu Glu Glu Leu Glu Lys Arg Leu Arg Gly Arg Ala Thr
 130 135 140
 Glu Thr Glu Glu Ser Leu Thr Lys Arg Leu Ala Gln Ala Lys Asn Glu
 145 150 155 160
 Leu Glu Tyr Ala Ala Gln Pro Gly Ser His Asp Lys Ile Val Val Asn
 165 170 175
 Asp Asp Leu Glu Lys Ala Tyr Lys Glu Leu Arg Asp Trp Ile Val Asp
 180 185 190
 Gly Gly Asn Phe Gly Ala Arg Gln
 195 200

<210> 10

<211> 2059

<212> DNA

<213> *Aspergillus fumigatus*

<400> 10

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 gcgccggtcg gagcgcatgt tgtcaacagc ctaatcaacg atgtcttcat tgaggagaag 120
 gttcgagcgc agaatcaggc agcgagcagt gcagctccta tctacaagaa ggaaaagtat 180
 actctgaaat ggaagcaagt aaaggatttc aatctgatat ttgtggtatg ttcacgccgc 240
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 cttggttgga tcgacaaact cttggataat gtttcgacca tattcatcga cttatataag 360
 gatgagctaa ggagcacacg ggctaggatt attgagtacc cattcgataa gtacttcgac 420
 cagcaggtgc gagagcttga ggacaatgct ggggctccta catcagaatc tctcgtagta 480
 gagatcaacg agagaaagga ccctcttgct tcatacagata acggcgggcc acctccgcca 540
 cccgtgcctg gtctgctgaa aggtatctga cgtcgataat ttttctctgc tagtgatcat 600
 attgctaact acctccgaag cgcaacgtcc agttgcgcag ggcgtggcga cctcggacga 660
 gggttcgcca ccccaaacc cagatctttc tcgatcgta acgcccattt caggatcatct 720
 attgaccgcg aaaggagggc ctgctggccg cgcctctcgt cgcgcacgca aagcggccaa 780
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 tggaaaaaag atgcgcaagt gggatgctga tggctttgcg gatgaggacg acggcaaggt 900
 cctcgattac tccgcccccg cagatggtga ggacgcaccg gctcctgtag tcgaggctgt 960
 tgcgcaggaa tcctggggac gccgaacagg caagggccaa tttgtgctga aagatctagg 1020

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ggatgaagtc cattccattc ttgagaatgc tgatcatgaa aagacaaaagt cttcctcgtc 1080
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gctgaagaag aacgttgcg cgaagcggc cgtccgtcta tgtcaaggcg tccagcgcga 1260
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caaccaagct ttcggcactg ggagaaacct cgatgggttc atcatcagta aatgtgatac 1920
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caatctgctg atgaagtga 2059

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<210> 11

<211> 1923

<212> DNA

<213> *Aspergillus fumigatus*

<400> 11

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tacttcgacc agcaggtgcg agagcttgag gacaatgctg gggctcctac atcagaatct 420
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aag 1923

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<210> 12

<211> 641

<212> PRT

<213> *Aspergillus fumigatus*

<400> 12

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Ser Lys Ser Tyr Ala Pro Val Gly Ala His Val Val Asn Ser Leu Ile
 20 25 30

Asn Asp Val Phe Ile Glu Glu Lys Val Arg Ala Gln Asn Gln Ala Ala
 35 40 45

Ser Ser Ala Ala Pro Ile Tyr Lys Lys Glu Lys Tyr Thr Leu Lys Trp
 50 55 60

Lys Gln Val Lys Asp Phe Asn Leu Ile Phe Val Ala Val Tyr Gln Ser
 65 70 75 80

Leu Leu His Leu Gly Trp Ile Asp Lys Leu Leu Asp Asn Val Ser Thr
 85 90 95

Ile Phe Ile Asp Leu Tyr Lys Asp Glu Leu Arg Ser Thr Arg Ala Arg
 100 105 110

Ile Ile Glu Tyr Pro Phe Asp Lys Tyr Phe Asp Gln Gln Val Arg Glu
 115 120 125

Leu Glu Asp Asn Ala Gly Ala Pro Thr Ser Glu Ser Leu Val Val Glu
 130 135 140

Ile Asn Glu Arg Lys Asp Pro Leu Val Ser Ser Asp Asn Gly Gly Pro
 145 150 155 160

Pro Pro Pro Pro Val Pro Val Ala Gln Gly Val Ala Thr Ser Asp Glu
 165 170 175

Gly Ser Pro Pro Gln Thr Pro Asp Leu Ser Arg Ser Ser Thr Pro Ile
 180 185 190

Ser Gly His Leu Leu Thr Ala Lys Gly Gly Pro Ala Gly Arg Ala Ser
 195 200 205

Arg Arg Ala Arg Lys Ala Ala Asn Ala Ser Ala Thr Ala Ser Ser Gly
 210 215 220

Asp Glu Ser Ile Arg Lys Gly Lys Thr Leu Lys Ser Gly Lys Lys Met
 225 230 235 240

Arg Lys Trp Asp Ala Asp Gly Phe Ala Asp Glu Asp Asp Gly Lys Val
 245 250 255

Leu Asp Tyr Ser Ala Pro Ala Asp Gly Glu Asp Ala Pro Ala Pro Val
 260 265 270

Val Glu Ala Val Ala Gln Glu Ser Trp Gly Arg Arg Thr Gly Lys Gly
 275 280 285

Gln Phe Val Leu Lys Asp Leu Gly Asp Glu Val His Ser Ile Leu Glu

290	295	300
Asn Ala Asp His Glu Lys Thr Lys Ser Ser Ser Ser Thr Gly Phe Val 305 310 315 320		
Gly Ser Gly Val Asn Ala Leu Gly Gly Phe Phe Arg Asn Ile Val Gly 325 330 335		
Gly Lys Val Leu Thr Glu Ala Asp Leu Glu Lys Pro Leu Lys Ala Met 340 345 350		
Glu Asp His Leu Leu Lys Lys Asn Val Ala Arg Glu Ala Ala Val Arg 355 360 365		
Leu Cys Gln Gly Val Gln Arg Glu Leu Val Gly Lys Lys Thr Gly Asn 370 375 380		
Phe Gln Ser Val Asp Ala Ala Leu Arg Ser Ala Met Glu Ser Ser Leu 385 390 395 400		
Arg Lys Ile Leu Thr Pro Thr Ser Ser Leu Asp Leu Leu Arg Glu Ile 405 410 415		
Asp Ala Val Arg Ser Pro Thr Ser Lys Gly Gln Ala Pro Arg Pro Tyr 420 425 430		
Val Ile Ser Ile Val Gly Val Asn Gly Val Gly Lys Ser Thr Asn Leu 435 440 445		
Gly Lys Ile Cys Tyr Phe Leu Leu Gln Asn Asn Tyr Arg Val Leu Ile 450 455 460		
Ala Ala Cys Asp Thr Phe Arg Ser Gly Ala Val Glu Gln Leu Arg Val 465 470 475 480		
His Ala Arg Asn Leu Lys Glu Leu Ser Thr Arg Glu Asn Ala Gly Glu 485 490 495		
Val Glu Leu Tyr Glu Lys Gly Tyr Gly Lys Asp Ala Ala Asn Val Ala 500 505 510		
Lys Asp Ala Val Glu Tyr Gly Ala Ala Asn His Phe Asp Val Val Leu 515 520 525		
Ile Asp Thr Ala Gly Arg Arg His Asn Asp Gln Arg Leu Met Ser Ser 530 535 540		
Leu Glu Lys Phe Ala Lys Phe Ala Lys Pro Asp Lys Ile Phe Met Val 545 550 555 560		
Gly Glu Ala Leu Val Gly Thr Asp Ser Val Met Gln Ala Arg Asn Phe 565 570 575		
Asn Gln Ala Phe Gly Thr Gly Arg Asn Leu Asp Gly Phe Ile Ile Ser 580 585 590		
Lys Cys Asp Thr Val Gly Asp Met Val Gly Thr Leu Val Ser Met Val 595 600 605		
His Ala Thr Gly Ile Pro Ile Val Phe Leu Gly Val Gly Gln His Tyr 610 615 620		

Gly Asp Leu Arg Gly Leu Ser Val Pro Trp Ala Val Asn Leu Leu Met
 625 630 635 640

Lys

<210> 13
 <211> 1564
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 13
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 aaattatggg ctgacctaga aggtgctcta acctactgaa cttctacgtt aatatgctaa 180
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 ataa 1564

<210> 14
 <211> 1380
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 14
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 aaattatggg ctgacctaga aggatataac ctgcacttcg aatcccccaa gaatgacaag 180
 ctacgcctgt tcgaactcgg agaccgagtc tacgaccaca tgcttctcct gcctcccaag 240
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```

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ggtgatggga agcagatgaa gacggtcaac caggaattcg ccaagcagct tactgcgtgg 840
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<210> 15

<211> 460

<212> PRT

<213> *Aspergillus fumigatus*

<400> 15

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Met Arg Trp Cys Leu Thr Leu Leu Ala Phe Cys Phe Leu Ala Val Val
  1              5              10              15

```

```

Arg Ala Leu Ser Ser Ser Gly Ser Arg Leu Leu Val Val Leu Glu Asp
      20              25              30

```

```

Ala Thr Glu Lys Glu Leu Tyr Ser Lys Leu Trp Ala Asp Leu Glu Gly
      35              40              45

```

```

Tyr Asn Leu Asp Phe Glu Ser Pro Lys Asn Asp Lys Leu Ser Leu Phe
      50              55              60

```

```

Glu Leu Gly Asp Arg Val Tyr Asp His Met Leu Leu Leu Pro Pro Lys
      65              70              75              80

```

```

Ser Lys Gly Tyr Gly Pro Ser Leu Thr Pro Lys Asn Ile Ile Asp Phe
      85              90              95

```

```

Met Asn Lys Asp Gly Asn Val Leu Leu Ala Leu Ser Gly Lys Ser Thr
      100              105              110

```

```

Thr Ala Ser Ala Ile Ser Ser Leu Leu Leu Glu Leu Asp Leu His Leu
      115              120              125

```

```

Pro Val Asp Arg Ser Ser Val Thr Val Asp His Phe Asn Tyr Asp Thr
      130              135              140

```

```

Leu Ser Ala Ser Asp Lys His Asp Val Leu Leu Leu His Arg Pro Gly
      145              150              155              160

```

```

Lys Leu Arg Ser Asp Thr Lys Ala Phe Phe Asp Gly Glu Gly Val Val
      165              170              175

```

```

Ala Phe Pro Arg Ala Val Pro His Thr Leu Gly Asp Ala Asn Pro Leu
      180              185              190

```

```

Ile Ala Pro Ile Leu Arg Ala Pro Ala Thr Ala Tyr Ser Tyr Asn Pro
      195              200              205

```

```

Lys Glu Asp Ala Ser Ser Val Glu Asp Val Ala Ala Thr Gly Ser Gln
      210              215              220

```

Leu Ala Leu Val Ser Ala Met Gln Ala Arg Asn Ser Ala Arg Phe Thr
 225 230 235 240
 Leu Leu Gly Ser Val Glu Ser Leu Gln Asp Gln Trp Phe Ser Ala Thr
 245 250 255
 Val Lys Ala Pro Gly Asp Gly Lys Gln Met Lys Thr Val Asn Gln Glu
 260 265 270
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 Thr Val Tyr Ser Thr Arg Phe Thr Thr Pro Asp Gln His Gly Ile Phe
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 Lys Leu Glu Val Thr Val Arg His Phe Ala His Asn Glu Tyr Pro Arg
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<212> DNA

<213> *Aspergillus fumigatus*

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<211> 2145

<212> DNA

<213> *Aspergillus fumigatus*

<400> 17

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<213> *Aspergillus fumigatus*

<400> 18

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Phe Gly Leu Ile Asn Ala Val Gln Glu Leu Arg Lys Asp Phe Pro Phe
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Leu Asn Ser Lys Asp Glu Lys Leu Glu Asn Glu Trp Leu Ser Gln Leu
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Leu Ser Thr Ala Asp Ile Ala Leu Trp Gly Ala Ile Arg Gly Asn Arg
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Val Ala Val Ala Ala Ile Lys Lys Gly Ser Leu Val Asn Val Thr Arg
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Trp Phe Tyr Phe Leu Glu Asp Leu Cys Pro Trp Ala Thr Ser Thr Leu
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Lys His Gly Lys Asn Pro Ala Val Gly Met Lys Lys Val Val Phe Gly
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Ser Thr Glu Gly Gln Asp Leu Ile Pro Val Glu Leu Val Asp Phe Asp
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Tyr Leu Leu Asn Lys Asp Thr Leu Gln Glu Asp Asp Val Leu Glu Asp
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Val Leu Asn Lys Asn Thr Glu Phe Arg Glu Asp Ala Val Ala Asp Cys
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Asn Val Ala Glu Leu Lys Glu Gly Asp Ile Ile Gln Phe Glu Arg Lys
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<210> 19

<211> 2639

<212> DNA

<213> *Aspergillus fumigatus*

<400> 19

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<212> DNA

<213> *Aspergillus fumigatus*

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<210> 21

<211> 809

<212> PRT

<213> *Aspergillus fumigatus*

<400> 21

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Tyr Tyr His Leu Asp Asn Asn Leu Cys Arg Asn Ala Leu Phe Leu Ala
      20              25              30

Gly Arg Leu His Ala Tyr Glu Pro Arg Thr Ala Glu Ala Ser Tyr Leu
      35              40              45

Leu Ala Leu Cys His Leu Gln Asn Gly Gln Val Lys Ala Ala Tyr Asp
      50              55              60

Tyr Ser Arg Asn Phe Gly Ser Arg Gly Thr His Leu Gly Cys Ser Tyr
      65              70              75              80

Val Phe Ala Gln Ala Cys Leu Asp Leu Gly Lys Tyr Leu Glu Gly Ile
      85              90              95

Thr Ala Leu Glu Arg Ser Lys Gly Leu Trp Ala Ser Lys Asn His Trp
      100             105             110

Asn Lys His Ser Glu Thr Arg Arg Gln His Leu Pro Asp Ala Ala Ala
      115             120             125

Val Phe Cys Leu Leu Gly Lys Leu Trp His Ala His Lys Asp Ile Asn
      130             135             140

Lys Ala Val Glu Cys Tyr Val Glu Ser Leu Lys Leu Asn Pro Phe Met
      145             150             155             160

Trp Asp Ala Phe Gln Gly Leu Cys Asp Thr Gly Val Asn Val Arg Val
      165             170             175

Ser Asn Ile Tyr Lys Leu Asn Ser Glu Leu Leu Ala Val Leu Ser Ser
      180             185             190

Ser Pro Gln Ala Asp Ala Glu Pro Ile Ser Asp Lys Ser Ala His Thr

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195					200					205					
Asn	Gly	Pro	Leu	Gln	Ala	Gln	Ala	Asn	Val	Asn	Pro	Ser	Ser	Asp	Pro
210					215					220					
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225					230					235					240
Ser	Ala	Leu	Trp	Glu	Lys	Leu	Asn	Gly	Ser	Thr	Val	Ser	Val	Ala	Ser
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Ser	Gly	Val	Pro	Ala	Ser	Ile	Val	His	Glu	Gly	Ala	Glu	Thr	Pro	Ser
			260					265					270		
Gly	Gln	Ser	Ser	Gly	Ser	Asp	Glu	Phe	Arg	Leu	Ala	Asn	Gly	Met	Asn
				275			280					285			
Gly	Ala	Asp	Ala	Ser	Trp	Asp	Pro	Pro	Leu	Ala	Pro	Ala	Arg	Lys	Asn
				290			295					300			
Arg	Thr	Ile	Gln	Ala	Ile	Ser	Gly	Glu	Tyr	Pro	Met	Asp	Pro	Pro	Pro
305					310					315					320
Lys	Met	Lys	Pro	Thr	Gly	Ile	Arg	Pro	Arg	Thr	Arg	Thr	Arg	Thr	Glu
				325					330					335	
Pro	Glu	Asp	Gln	Ile	Ser	Ala	Gln	Ile	Asp	Arg	Glu	Ala	Thr	Asn	Ala
				340				345					350		
Pro	Arg	Val	Gly	Asp	Arg	Lys	Arg	Thr	Val	Ser	Gly	Gln	Val	Ala	His
				355				360				365			
Pro	Pro	Thr	Ser	Gln	Pro	Thr	Glu	Pro	Gly	Ala	Pro	Gln	Arg	Arg	Ser
				370			375					380			
Val	Arg	Leu	Phe	Asn	Gln	Ile	Lys	Pro	Thr	Thr	Ser	Lys	Leu	Ser	Ala
385					390					395					400
Ser	Ala	Leu	Gly	Val	Lys	Asp	Ala	Arg	Glu	Val	Lys	Lys	Ala	Lys	Ala
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Thr	Gly	Thr	Lys	Gly	Arg	Thr	Thr	Thr	Thr	Thr	Met	Gly	Arg	Val	Val
			420					425					430		
Ser	Gly	Ser	Arg	Lys	His	Ala	Ser	Glu	His	His	Asp	Ala	Asp	Gly	Lys
				435			440					445			
Asp	Gly	Arg	Ser	Val	Pro	Ser	Ala	His	Thr	His	Ala	Ile	Ser	Lys	Gly
				450			455					460			
Ala	Ala	Gln	Glu	Arg	Ser	Lys	Glu	Ile	Glu	Ala	Leu	Thr	Trp	Leu	Leu
465					470					475					480
Glu	Leu	Phe	Ser	Lys	Leu	Ala	Ser	Gly	Phe	Phe	Ala	Leu	Cys	Arg	Tyr
				485					490					495	
Arg	Cys	Pro	Glu	Ser	Ile	Gln	Ile	Phe	Asn	Ser	Leu	Ser	Gln	Gly	Gln
			500					505					510		
Arg	Glu	Thr	Pro	Trp	Val	Leu	Ala	Gln	Ile	Gly	Arg	Ala	Tyr	Tyr	Glu
				515			520					525			

Gln Ala Met Tyr Ser Glu Ala Glu Lys Tyr Phe Tyr Arg Val Lys Thr
 530 535 540
 Met Ala Pro Ser Arg Leu Glu Asp Met Glu Ile Tyr Ser Thr Val Leu
 545 550 555 560
 Trp His Leu Lys Asn Asp Val Glu Leu Ala Tyr Leu Ala His Glu Leu
 565 570 575
 Met Glu Thr Asp Arg Leu Ser Pro Gln Ala Trp Cys Ala Ile Gly Asn
 580 585 590
 Ser Phe Ser His Gln Arg Asp His Asp Gln Ala Leu Lys Cys Phe Lys
 595 600 605
 Arg Ala Thr Gln Leu Asp Pro Gln Phe Ala Tyr Gly Phe Thr Leu Gln
 610 615 620
 Gly His Glu Tyr Val Ala Asn Glu Glu Tyr Asp Lys Ala Leu Asp Ala
 625 630 635 640
 Tyr Arg His Gly Ile Ser Ala Asp Ser Arg His Tyr Asn Ala Trp Tyr
 645 650 655
 Gly Leu Gly Thr Val Tyr Asp Lys Met Gly Lys Leu Asp Phe Ala Glu
 660 665 670
 Gln His Phe Arg Asn Ala Ala Ser Ile Asn Pro Thr Asn Ala Val Leu
 675 680 685
 Ile Cys Cys Ile Gly Leu Val Leu Glu Lys Met Asn Asn Pro Lys Ala
 690 695 700
 Ala Leu Val Gln Tyr Gly Arg Ala Cys Ser Leu Ala Pro His Ser Val
 705 710 715 720
 Leu Ala Arg Phe Arg Lys Ala Arg Ala Leu Met Lys Leu Gln Glu Leu
 725 730 735
 Lys Leu Ala Leu Ser Glu Leu Lys Ile Leu Lys Asp Met Ala Pro Asp
 740 745 750
 Glu Ala Asn Val His Tyr Leu Leu Gly Lys Leu Tyr Lys Met Leu His
 755 760 765
 Asp Lys Ala Asn Ala Ile Lys His Phe Thr Thr Ala Leu Asn Leu Asp
 770 775 780
 Pro Lys Ala Ala Gln Tyr Ile Lys Asp Ala Met Glu Ser Leu Asp Asp
 785 790 795 800
 Asp Glu Glu Asp Asp Glu Asp Met Ser
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<210> 22

<211> 1836

<212> DNA

<213> *Aspergillus fumigatus*

<400> 22

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gagaacctca tggcaaaggc cctggatata tcccttgta caaccgggtg gaagtgggag 180
cttcagtatg atgttcttca actcagtgat cgcgtcaatg agctgaactc gctacatggc 240
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gagacgtacg aattcaacca ccttctgcgc aacgttaaag aagcgaccct ggtactacgc 360
aatatgggtcc ttctgaaaga gaatgcctac tatgtgtcac ggtacgcgaa aggcctgctc 420
cgagacttcc tcgtcattat gatcaacttg cccaatcagc ctcgtctcaa cgagatcaag 480
aacgacgctt tggacattgc agaggaggtc accaagtta tgaagaccga tccggaagat 540
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gcactctggg ctctcaccca tttctccact gaattagacg agccagaggc gaaccgggca 660
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```

<210> 23

<211> 1836

<212> DNA

<213> *Aspergillus fumigatus*

<400> 23

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gagaacctca tggcaaaggc cctggatata tcccttgta caaccgggtg gaagtgggag 180
cttcagtatg atgttcttca actcagtgat cgcgtcaatg agctgaactc gctacatggc 240
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gagacgtacg aattcaacca ccttctgcgc aacgttaaag aagcgaccct ggtactacgc 360
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```

```

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<210> 24

<211> 611

<212> PRT

<213> *Aspergillus fumigatus*

<400> 24

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Ala His Tyr Gly Leu Gln Ser Gly Ile Pro Asp Glu Val Asp Phe Ala
  1              5              10              15

```

```

Leu Tyr His Leu Val Gln Ile Ser Asn Gln Arg Trp Asp Lys Phe Lys
          20              25              30

```

```

Phe Glu Gly Phe Pro Leu Leu Ala Glu Asn Leu Met Ala Lys Ala Leu
      35              40              45

```

```

Asp Ile Ser Leu Val Thr Thr Gly Val Lys Trp Glu Leu Gln Tyr Asp
      50              55              60

```

```

Val Leu Gln Leu Ser Asp Arg Val Asn Glu Leu Asn Ser Leu His Gly
      65              70              75              80

```

```

Thr Arg Asp Leu Leu Glu Lys Ile Lys Gln Met Pro Val Thr Leu Pro
          85              90              95

```

```

Glu Asp Thr Leu Glu Thr Tyr Glu Phe Asn His Leu Leu Arg Asn Val
      100              105              110

```

```

Lys Glu Ala Thr Leu Val Leu Arg Asn Met Val Leu Leu Lys Glu Asn
      115              120              125

```

```

Ala Tyr Tyr Val Ser Arg Tyr Ala Lys Gly Leu Leu Arg Asp Phe Leu
      130              135              140

```

```

Val Ile Met Ile Asn Leu Pro Asn Gln Pro Arg Leu Asn Glu Ile Lys
      145              150              155              160

```

```

Asn Asp Ala Leu Asp Ile Ala Glu Glu Val Thr Lys Phe Met Lys Thr
          165              170              175

```

```

Asp Pro Glu Asp Pro Leu Trp Ile Ser Leu Leu Asn Cys Leu Gly Ser
          180              185              190

```

```

Ser Asp Arg Ala His Val Val Arg Ala Leu Trp Ala Leu Thr His Phe
      195              200              205

```

```

Ser Thr Glu Leu Asp Glu Pro Glu Ala Asn Arg Ala Met Glu Arg Ile
      210              215              220

```

Pro Lys Glu Thr Leu Gln Gln Leu Tyr Phe His Thr Leu Leu Asp Leu
 225 230 235 240
 Asp Lys Asp Ile Leu Ser Gly Ala Leu Asp Phe Trp Tyr Gln Tyr Thr
 245 250 255
 Leu Ser Ser Glu Asn Ile Glu Thr Leu Ile Glu Val Phe Asn Leu Pro
 260 265 270
 Thr Val Phe Val Pro Arg Met Val Ala Leu Leu Thr His Glu Gly Arg
 275 280 285
 Pro Asn Lys Lys Glu Thr Val Leu Gln Glu Glu Lys Val Ala Pro Pro
 290 295 300
 Pro Ser Asp Ile Pro Arg Val Pro Pro Glu Leu Met Lys Glu Leu Met
 305 310 315 320
 Glu Leu Ser Glu Pro Glu Arg Ser Ser Arg Trp Leu Arg Cys Cys Phe
 325 330 335
 Val Glu Asp Leu Glu Cys Glu Ile Thr Gln Ile Ala Leu Trp Gln Ala
 340 345 350
 Tyr Gln Ser Arg Phe Ala Asp Pro Arg Leu Pro Gly Gly Gly Val Leu
 355 360 365
 Pro Ala Ala Glu Phe Ile Lys Asn Val Ser Thr Thr Phe Thr Asn Ala
 370 375 380
 Gln Ala Gln Val Ile Asn Gly Pro Gly Ala Ala Thr Lys Phe Ile Ile
 385 390 395 400
 Lys Gly Ile Arg Pro Leu Glu Thr Ala Tyr Thr Phe Glu Gly Phe Pro
 405 410 415
 Tyr Ile Tyr Cys Lys Trp Ala Asp Asn Ser Lys Pro Ser Lys Thr Cys
 420 425 430
 Gln Arg Ala Phe Lys Ser Pro Ala Glu Leu Arg His His Val Phe Thr
 435 440 445
 Glu His Met Asn Leu Lys Pro Thr Glu Thr Pro Gly His Tyr Asn Leu
 450 455 460
 Glu Lys Ala Glu Ser Pro Val His Thr Cys Leu Trp Asp Asn Cys Thr
 465 470 475 480
 Lys Phe Arg Ser Ser Gly Pro Ser Ala Asn Thr Ala Met Val Ala Gly
 485 490 495
 His Val Ser Ala His Leu Pro Glu Glu Arg Ala Pro Asp Ala Glu Pro
 500 505 510
 Pro Thr Ser Lys Arg Ala Val Leu Gln Glu Arg Ile Val Arg Lys Trp
 515 520 525
 Tyr Tyr Leu Asp Thr Pro Val Asn Glu Arg Gly Glu Pro Phe Gly Val
 530 535 540
 Ala Tyr Lys Ala Ala Leu Val Leu Arg Asn Leu Ala Arg Asn Leu Pro

545 550 555 560
 Thr Gly Ile Ala Pro Gln Tyr Asn Gly Leu Ser Trp Lys Lys Ala Val
 565 570 575
 Phe Leu Ser His Arg Pro Lys Ile Ile Glu Ala Trp Asp Arg Asn Arg
 580 585 590
 Ser Leu Arg Lys Glu Leu Thr Glu Leu Ile Met Val Ile Glu Lys Glu
 595 600 605
 Asp Tyr Tyr
 610

<210> 25

<211> 1542

<212> DNA

<213> *Aspergillus fumigatus*

<400> 25

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ggagccaaga ccgagtttac ggaaacggag accaaggtcc tcagtgtacc ccagggcgct 780
gctctgcaga ctgattcgga ggatgagact ttggaagtct tgatgaccga cttggatgag 840
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<210> 26

<211> 1479

<212> DNA

<213> *Aspergillus fumigatus*

<400> 26

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cagcccgcgg gtctgaaggc tgttccggag gagatctgga aggacatgtt ggatctcgtc 240
aattgccagg tcctctcgat tgtttcgtca gaggatgtgg acgcctacct gctctccgag 300

```



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<210> 27

<211> 493

<212> PRT

<213> *Aspergillus fumigatus*

<400> 27

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Phe Ala Gly Thr Pro Ser Leu Thr Ile Asn Tyr Glu Ala Thr Gln Asp
      20                25                30

Leu Asp Ser Thr Asn Ala Phe Glu Gly Pro Glu Lys Leu Leu Glu Val
      35                40                45

Trp Phe Ala Pro Ser Ala Gln Glu Leu Gly Pro Ala Gln Pro Ala Gly
      50                55                60

Leu Lys Ala Val Pro Glu Glu Ile Trp Lys Asp Met Leu Asp Leu Val
      65                70                75                80

Asn Cys Gln Val Leu Ser Ile Val Ser Ser Glu Asp Val Asp Ala Tyr
      85                90                95

Leu Leu Ser Glu Ser Ser Met Phe Val Trp Pro His Lys Leu Ile Leu
      100                105                110

Lys Thr Cys Gly Thr Thr Thr Leu Leu Ser Gly Leu Pro Arg Ile Leu
      115                120                125

Glu Ile Ala Ala Leu Phe Gly Gly Phe Pro Lys Ser Thr Ala Pro Ser
      130                135                140

Arg Gly Ile Ser Val Ala Ala Ala Pro Tyr Arg Val Phe Tyr Ser Arg
      145                150                155                160

Lys Asn Phe Leu Phe Pro Asp Arg Gln Arg Gly Pro His Arg Ser Trp
      165                170                175

```

Arg Asp Glu Val Arg Thr Met Asp Lys Leu Phe Leu Asn Gly Ser Ala
 180 185 190
 Tyr Met Ile Gly Lys Met Asn Gly Glu His Trp Tyr Leu Tyr Leu Thr
 195 200 205
 Glu Pro His Thr Met Leu Thr Pro Pro Thr Ser Pro Gly Ala Lys Thr
 210 215 220
 Glu Phe Thr Glu Thr Glu Thr Lys Val Leu Ser Val Pro Gln Gly Ala
 225 230 235 240
 Ala Leu Gln Thr Asp Ser Glu Asp Glu Thr Leu Glu Val Leu Met Thr
 245 250 255
 Asp Leu Asp Glu Glu Asn Ala Lys Gln Phe Tyr Leu Glu Asn Ala Thr
 260 265 270
 Ala Val Ala Glu Asn Arg Tyr Arg Asn Ser Asn Ser Glu Lys Ser Gly
 275 280 285
 His Val Asp Val Phe Ser Asn Thr Ser Ser Asp Ile Ser Asp Phe Asp
 290 295 300
 Ser Asp Gly Ser Gln Val Leu Pro Pro Glu Leu Thr Thr Glu Gly His
 305 310 315 320
 Ala Leu Gly Thr Val Val Ser Glu Ala Cys Gly Leu Ser Ser Val Tyr
 325 330 335
 Pro Lys Glu Lys Tyr Pro Asp Ser Arg Ile Asp Ala Tyr Leu Phe Thr
 340 345 350
 Pro Cys Gly Phe Ser Ala Asn Gly Val Ile Pro Pro Pro Glu Gly Lys
 355 360 365
 Ala Gly Thr His Tyr Phe Thr Val His Val Thr Pro Glu Pro His Cys
 370 375 380
 Ser Tyr Ala Ser Phe Glu Thr Asn Val Pro His Ser Gln Asn Gly Gln
 385 390 395 400
 Thr Thr Ala Gly Ile Ile Lys Gln Val Val Asp Ile Phe Lys Pro Gly
 405 410 415
 Arg Phe Ser Val Thr Leu Phe Glu Ala Lys Pro Ala Leu Ser Gln Val
 420 425 430
 Glu Asp Glu Trp Lys Glu Ala Lys Tyr Leu Ala Ala Arg Arg Thr Ala
 435 440 445
 Lys Met Glu His Val Glu Gly Tyr Arg Arg Val Asp Arg Ile Val His
 450 455 460
 Asp Leu Asp Gly Tyr Glu Leu Val Phe Arg Tyr Tyr Glu Arg Leu Asp
 465 470 475 480
 Trp Lys Gly Gly Ala Pro Arg Leu Gly Glu Glu Arg Ser
 485 490

<210> 28
 <211> 637
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 28
 atgggtcgcg ttagaaccac ggtaagttac agatgaagca tcatgagtta tcttcaaaaa 60
 agccccaata gagtatcatt tctgacgaaa tgggtttttc ttcaatagac agtcaagagg 120
 tccgccaaag tcatcatcga gcgctactac cccaagttga cgctcgactt tgagaccaac 180
 aagcgtcttt gcgatgagat cgctatcatt gcctccaagc gccttcgcaa caaggtgggc 240
 aatccatcac tgagccgtac aacagtcgga atttgacttg ctgacgaaaa ctgatttgc 300
 ggttacacca cccaccttat gaagcgtatc cagcgtggcc ctgtccgcgg tatctcttc 360
 aagctgcagg aggaggagcg tgagcgcaag gatcagtagc ttcctgagggt ttccgctctg 420
 gatgtttccc agaccgagtc cggccagctc gatgtcgatg ccgacacca ggaccttctc 480
 aagtccatgg gcgtaagttc tgttctcaac gcggttggtc gtggttttaa agcagtcctg 540
 taacttatat tgcccactac agttcgacaa tctcaaggtc aacgttgtca acgtctcca 600
 acatcagggt caggagcgcc cccgccgctt ccggtag 637

<210> 29
 <211> 417
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 29
 atgggtcgcg ttagaaccac gacagtcaag aggtccgccca aggtcatcat cgagcgctac 60
 taccccaagt tgacgctcga ctttgagacc aacaagcgtc tttgcatga gatcgctatc 120
 attgcctcca agcgccttcg caacaagatt gctggttaca ccaccacct tatgaagcgt 180
 atccagcgtg gccctgtccg cggtatctct tccaagctgc aggaggagga gcgtgagcgc 240
 aaggatcagt acgttcctga ggtttccgct ctggatgttt ccagaccga gtccggccag 300
 ctgatgtcgc atgccgacac caaggacctt ctcaagtcca tgggcttcga caatctcaag 360
 gtcaacggtt tcaacgtctc ccaacatcag gttcaggagc gccccgccg cttccgg 417

<210> 30
 <211> 139
 <212> PRT
 <213> *Aspergillus fumigatus*

<400> 30
 Met Gly Arg Val Arg Thr Lys Thr Val Lys Arg Ser Ala Lys Val Ile
 1 5 10 15
 Ile Glu Arg Tyr Tyr Pro Lys Leu Thr Leu Asp Phe Glu Thr Asn Lys
 20 25 30
 Arg Leu Cys Asp Glu Ile Ala Ile Ile Ala Ser Lys Arg Leu Arg Asn
 35 40 45
 Lys Ile Ala Gly Tyr Thr Thr His Leu Met Lys Arg Ile Gln Arg Gly
 50 55 60
 Pro Val Arg Gly Ile Ser Phe Lys Leu Gln Glu Glu Glu Arg Glu Arg
 65 70 75 80
 Lys Asp Gln Tyr Val Pro Glu Val Ser Ala Leu Asp Val Ser Gln Thr
 85 90 95
 Glu Ser Gly Gln Leu Asp Val Asp Ala Asp Thr Lys Asp Leu Leu Lys
 100 105 110

Ser Met Gly Phe Asp Asn Leu Lys Val Asn Val Val Asn Val Ser Gln
 115 120 125

His Gln Val Gln Glu Arg Pro Arg Arg Phe Arg
 130 135

<210> 31

<211> 1035

<212> DNA

<213> *Aspergillus fumigatus*

<400> 31

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gtctggatac ggtgggtttac aggtactgat ccgggaacag gaacaagcgc ttgtcgaagg 120
gcaagaaggg tgtaaagaag aggaccgttg atcctttctc caggaaggac gaatactctg 180
ttaaggatat tgcacgtgga ctgtgtaagt cgaccgcagc taatctatat caggcgcctt 240
ccactttcca gatcagagag tatgttgac gcatatgat tccaatgcag gataaaggcg 300
attcacaatg gtagtggaga ttatgctgac tgaattatag tgcgggaag actctggtca 360
accgcaccag tgggtctcaag aacgccaatg actccctgaa gggtcgaatt ttcgaggtct 420
cgctggctga cctgcagaat gatgaagacc atgctttccg caaggttaag cttcgtgtgg 480
acgaggttca gggcaagaac tggttgacca acttccacgg tcttgatttc acaaccgaca 540
aattgcgac cctcgtgcgc aagtggcagt cgctgatcga agccatgtca ctgtgaagac 600
gaccgatgat tatctccttc ggctttttgc tatcgcttc accaagagac gcccgacca 660
gattaagaag accacatatg ctctgtcttc tcaaactcgt gccatccgca agaagatgat 720
tgaaatcatg cagagggagg cagccagctg ctctctcgt cagctcactc acaagctcat 780
tccagaggtc attggtcgtg agatcgagaa ggctaccag ggaatctatc ctttgcagaa 840
tgtgtgtgac cctgttattc ttactcggga tgaagactaa ctgcaatcta ggtccatatt 900
cgcaaggtca agcttcttaa ggctcccaag ttcgacctgg gtgcaactgt gaatctgcac 960
ggtgaatcta caaccgatga taagggccac aaggctcgaga gagagttoaa ggagcaggtt 1020
ctcgaaagcg ttttaa 1035
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<210> 32

<211> 768

<212> DNA

<213> *Aspergillus fumigatus*

<400> 32

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gttgatcctt tctccaggaa ggacgaatac tctgttaagg cgccttcac tttccagatc 120
agagatgtcg ggaagactct ggtcaaccgc accagtggtc tcaagaacgc caatgactcc 180
ctgaagggtc gaattttcga ggtctcgtg gctgacctgc agaagatga agaccatgct 240
ttccgcaagg ttaagcttcg tgtggacgag gttcagggca agaactgttt gaccaacttc 300
cacggtcttg atttcacaac cgacaaattg cgatccctcg tgcgcaagtg gcagtcgctg 360
atcgaagcca atgtcactgt gaagacgacc gatgattatc tccttcggct ttttgctatc 420
gccttcacca agagacgccc gaaccagatt aagaagacca catatgctcg ttcttctcaa 480
atccgtgcca tccgcaagaa gatgattgaa atcatgcaga gggaggcagc cagctgctct 540
ctcgctcagc tcactcacia gctcattcct gaggtcattg gtcgtgagat cgagaaggct 600
acccagggaa tctatccttt gcagaatgtc catattcgca aggtcaagct tcttaaggct 660
cccaagttcg acctgggtgc actgctgaat ctgcacggtg aatctacaac cgatgataag 720
ggccacaagg tcgagagaga gttcaaggag caggttctcg aaagcgtt 768
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<210> 33

<211> 256

<212> PRT

<213> *Aspergillus fumigatus*

<400> 33

Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Val
 1 5 10 15

Lys Lys Arg Thr Val Asp Pro Phe Ser Arg Lys Asp Glu Tyr Ser Val
 20 25 30

Lys Ala Pro Ser Thr Phe Gln Ile Arg Asp Val Gly Lys Thr Leu Val
 35 40 45

Asn Arg Thr Ser Gly Leu Lys Asn Ala Asn Asp Ser Leu Lys Gly Arg
 50 55 60

Ile Phe Glu Val Ser Leu Ala Asp Leu Gln Asn Asp Glu Asp His Ala
 65 70 75 80

Phe Arg Lys Val Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Cys
 85 90 95

Leu Thr Asn Phe His Gly Leu Asp Phe Thr Thr Asp Lys Leu Arg Ser
 100 105 110

Leu Val Arg Lys Trp Gln Ser Leu Ile Glu Ala Asn Val Thr Val Lys
 115 120 125

Thr Thr Asp Asp Tyr Leu Leu Arg Leu Phe Ala Ile Ala Phe Thr Lys
 130 135 140

Arg Arg Pro Asn Gln Ile Lys Lys Thr Thr Tyr Ala Arg Ser Ser Gln
 145 150 155 160

Ile Arg Ala Ile Arg Lys Lys Met Ile Glu Ile Met Gln Arg Glu Ala
 165 170 175

Ala Ser Cys Ser Leu Ala Gln Leu Thr His Lys Leu Ile Pro Glu Val
 180 185 190

Ile Gly Arg Glu Ile Glu Lys Ala Thr Gln Gly Ile Tyr Pro Leu Gln
 195 200 205

Asn Val His Ile Arg Lys Val Lys Leu Leu Lys Ala Pro Lys Phe Asp
 210 215 220

Leu Gly Ala Leu Leu Asn Leu His Gly Glu Ser Thr Thr Asp Asp Lys
 225 230 235 240

Gly His Lys Val Glu Arg Glu Phe Lys Glu Gln Val Leu Glu Ser Val
 245 250 255

<210> 34

<211> 614

<212> DNA

<213> *Aspergillus fumigatus*

<400> 34

cctgtcggag atgatcaaag gcagcacctc gaattttcga ggaacactgc gaatagtttc 60

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aatcatgtat atggacccat tttcccgta ccagaagcaa ttatatgtaa gtgggtttttg 120
cttctggcgg aacggtcctg tgttgggaaa ttgacggcta tcaatagcgc ctgctaaacg 180
ggttatgtcc ctcaaagaac cgacgttgaa aatgtccaag tcccatgccg acagacgctc 240
aaggatcatt cttacggatt cgcccgagaa aatctccaaa aagatcaatg ctgcgctcac 300
agactcgga ttaaccatta catatgaccc agtccgtcga cctggagtgg cgaatttaat 360
agagatcttg agtcacttcg atggacgaac ttgcatgag attgccatgg aataccgttc 420
agccagtctt cgcgctctaa aggaacatct ggccagaacg ttgtccaatc atcttgagcc 480
aataagagag aagtatctct cactttagg agatcagact gactaccttg attctatagc 540
agaacagggt tctgaagccg cgcgggcaac cgctgaattg acaatggagc aagtcaaagt 600
cgctatgggc ttaa                                     614

```

<210> 35

<211> 552

<212> DNA

<213> *Aspergillus fumigatus*

<400> 35

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cctgtcggag atgatcaaag gcagcacctc gaattttcga ggaacactgc gaatagtttc 60
aatcatgtat atggacccat tttcccgta ccagaagcaa ttatatcgcc tgctaaacgg 120
gttatgtccc tcaaagaacc gacgttgaaa atgtccaagt cccatgccga cagacgctca 180
aggatcattc ttacggattc gcccgcagaa atctccaaaa agatcaatgc tgcgctcaca 240
gactcggaat taaccattac atatgaccca gtccgtcgac ctggagtggc gaatttaata 300
gagatcttga gtcacttcga tggacgaact tgcatgaga ttgccatgga ataccgttca 360
gccagtcttc gcgctctaaa ggaacatctg gccagaacgt tgtccaatca tcttgagcca 420
ataagagaga agtatctctc actttagga gatcagactg actaccttga ttctatagca 480
gaacagggtt ctgaagccgc gcgggcaac gctgaattga caatggagca agtcaaagtc 540
gctatgggct ta                                     552

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<210> 36

<211> 184

<212> PRT

<213> *Aspergillus fumigatus*

<400> 36

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Pro Val Gly Asp Asp Gln Arg Gln His Leu Glu Phe Ser Arg Asn Thr
 1             5             10             15

Ala Asn Ser Phe Asn His Val Tyr Gly Pro Ile Phe Pro Ser Pro Glu
      20             25             30

Ala Ile Ile Ser Pro Ala Lys Arg Val Met Ser Leu Lys Glu Pro Thr
      35             40             45

Leu Lys Met Ser Lys Ser His Ala Asp Arg Arg Ser Arg Ile Ile Leu
 50             55             60

Thr Asp Ser Pro Ala Glu Ile Ser Lys Lys Ile Asn Ala Ala Leu Thr
 65             70             75             80

Asp Ser Glu Leu Thr Ile Thr Tyr Asp Pro Val Arg Arg Pro Gly Val
      85             90             95

Ala Asn Leu Ile Glu Ile Leu Ser His Phe Asp Gly Arg Thr Cys Asp
      100            105            110

Glu Ile Ala Met Glu Tyr Arg Ser Ala Ser Leu Arg Ala Leu Lys Glu
      115            120            125

His Leu Ala Arg Thr Leu Ser Asn His Leu Glu Pro Ile Arg Glu Lys

```

130

135

140

Tyr Leu Ser Leu Val Gly Asp Gln Thr Asp Tyr Leu Asp Ser Ile Ala
145 150 155 160

Glu Gln Gly Ser Glu Ala Ala Arg Ala Asn Ala Glu Leu Thr Met Glu
165 170 175

Gln Val Lys Val Ala Met Gly Leu
180

<210> 37

<211> 819

<212> DNA

<213> *Aspergillus fumigatus*

<400> 37

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actcaggtac ggaactcgaa actacgctat aatgaggctt tactcgtgat ttggatgttg 120
acaataatgt tcctagaccg agagtctgtt tcacacctat gcgcagtatg catcgatgac 180
gaagctgcct ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct 240
tcttgaaaag gtgtgcactt tgaggccctc tagtccagcc caacagacga tcatgctgac 300
acgatccgat catagcgtga agccctcatc tcccagctct cccgtctcct tgactccgaa 360
gccactctta ccgcatctgc cctgaaacag agcaatcttg cccgcaatcg cgaagtcctc 420
caggatcatc gccgcgaatt gcagcgccctg aacgccgcaa tcgccgagtc ccgcgaccga 480
gccaatcttc tgtctaacgt ccgctccgac attgatgcct accgcaattc aaaccccgcc 540
gcggctgagg cagactacat gctcgaggag cgggggtcgta tagatgaaag ccataacatg 600
atagatggtg tcctaagcca ggcgtatgca atcaacgaga gttttgggct acaacgtgaa 660
accctggcca gcatcaatcg ccgtatcgtc ggtgctgcca ataaggtacc aggaatgaat 720
gcattgattg gtaagattgg gacgaagagg agacgtgacg caatcatctt gggggctttc 780
atcggctttt gtttcttgat ggtgttcttc ttccgatga 819

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<210> 38

<211> 681

<212> DNA

<213> *Aspergillus fumigatus*

<400> 38

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atggcaactt cgactgggac cggatgggct cagctccggc agcaagcccg ttcgcttgag 60
actcagaccg agagtctgtt tcacacctat gcgcagtatg catcgatgac gaagctgcct 120
ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct tcttgaaaag 180
cgtgaagccc tcatctccca gctctcccgct ctctctgact ccgaagccac tcttaccgca 240
tctgccctga aacagagcaa tcttgcccgcc aatcgcgaa tccctccagga tcatcgccgc 300
gaattgcagc gcctgaacgc cgcaatcgcc gagtcccgcg accgagccaa tcttctgtct 360
aacgtccgct ccgacattga tgcctaccgc aattcaaacc ccgccgcggc tgaggcagac 420
tacatgctcg aggagcgggg tcgtatagat gaaagccata acatgataga tgggtgccta 480
agccaggcgt atgcaatcaa cgagagtttt gggctacaac gtgaaaccct ggccagcatc 540
aatcgccgta tcgtcggtgc tgccaataag gtaccaggaa tgaatgcatt gattggtaag 600
attgggacga agaggagacg tgacgcaatc atcttggggg ctttcatcgg cttttgtttc 660
ttgatggtgt tcttcttccg a 681

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<210> 39

<211> 227

<212> PRT

<213> *Aspergillus fumigatus*

<400> 39

Met Ala Thr Ser Thr Gly Thr Gly Trp Ala Gln Leu Arg Gln Gln Ala
 1 5 10 15
 Arg Ser Leu Glu Thr Gln Thr Glu Ser Leu Phe His Thr Tyr Ala Gln
 20 25 30
 Tyr Ala Ser Met Thr Lys Leu Pro Pro Lys Pro Ser Glu Glu Glu Gln
 35 40 45
 Arg Ile Glu Ser Gln Leu Lys Asp Leu Leu Glu Lys Arg Glu Ala Leu
 50 55 60
 Ile Ser Gln Leu Ser Arg Leu Leu Asp Ser Glu Ala Thr Leu Thr Ala
 65 70 75 80
 Ser Ala Leu Lys Gln Ser Asn Leu Ala Arg Asn Arg Glu Val Leu Gln
 85 90 95
 Asp His Arg Arg Glu Leu Gln Arg Leu Asn Ala Ala Ile Ala Glu Ser
 100 105 110
 Arg Asp Arg Ala Asn Leu Leu Ser Asn Val Arg Ser Asp Ile Asp Ala
 115 120 125
 Tyr Arg Asn Ser Asn Pro Ala Ala Ala Glu Ala Asp Tyr Met Leu Glu
 130 135 140
 Glu Arg Gly Arg Ile Asp Glu Ser His Asn Met Ile Asp Gly Val Leu
 145 150 155 160
 Ser Gln Ala Tyr Ala Ile Asn Glu Ser Phe Gly Leu Gln Arg Glu Thr
 165 170 175
 Leu Ala Ser Ile Asn Arg Arg Ile Val Gly Ala Ala Asn Lys Val Pro
 180 185 190
 Gly Met Asn Ala Leu Ile Gly Lys Ile Gly Thr Lys Arg Arg Arg Asp
 195 200 205
 Ala Ile Ile Leu Gly Ala Phe Ile Gly Phe Cys Phe Leu Met Val Phe
 210 215 220
 Phe Phe Arg
 225

<210> 40

<211> 1601

<212> DNA

<213> *Aspergillus fumigatus*

<400> 40

atgtcacaaa atcgacctgg ggtgttctcg aatctgcgca tgggtggtaa ggaacatcca 60
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 ctttccgacc atacagaagt cgctcgcgag aagggtccagg atggactgac aggggaaact 180
 aaggagattt cgtactcaca atgtaaaatc gtcggcaatg gatcgtttgg tgtcgtcttt 240
 cagacgaaaa tgatgccaag cggcgaggat gctgccatta agagggtcct tcaagacaag 300
 cgcttcaaag tatgtgtaca ttataagggc aattgccctc gctgccaac ccaaagatac 360
 tgtcgctgac gagataccag aatcgagaac tgcagattat gcggattgtt cgccatccta 420
 acatcgtaga attgaaagcc ttctattact cgaacggcga gagggtatgc gactctcctt 480


```

tgtctcccca ttctgttctag tttgccgttt gctgactacc ctaccattgt ctttcacaga 540
aggatgaagt gtacctaaac ctctgttctcg aatacgtacc agaaaccgtg tatcgggcgt 600
cgcggtactt taataaactc aaaacgacta tgccaatgtt ggaagtcaag ctgtatatct 660
atcaattgtt ccgttccctg gcatacatcc attcacaagg catctgccac cgtgacatca 720
agccccagaa tctcttactt gatccatcca ccggcatcct caaactctgc gactttgggt 780
cggccaagat tctggttagag aatgagccca acgtttccta tatctgttcc cgctactatc 840
gtgcgcggga attgatcttt ggcgccacta attacacaac aaagatcggt aagtcttgac 900
tgattcctcc ttcaagtttg gtactgtcat gctgacgac gtcaagacgt gtggtccacg 960
ggttggtgta tggctgaact catgcttggg cagccattgt tccctggaga gtcgggaatt 1020
gaccaactgg tggaaatcat caaggttctt ggaacccta ctcgggagca gatccgcacc 1080
atgaacccaa actatagga gcacaaattc cctcaaatca agccacaccc attcaacaag 1140
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ccggagagct cctcacgagg ccattgatct gatctcagct ttgctagaat acacgccgac 1260
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caatacgcga ctgcccgaact ctcgccaccc tgggtggcgt gctagagacc tccccaatct 1380
ctttgatctt tccagacatg gtttggtgtc acttgaggcc caaattcatt cttccagatg 1440
gcttattcgc tgatcaactct tttgtagaac tttctattgc acctgcattg aacagccggc 1500
tggttcccc tcatgcacgc gccgctctcg aggccgggg gctagacatt gacaacttca 1560
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<210> 41

<211> 1182

<212> DNA

<213> *Aspergillus fumigatus*

<400> 41

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gtcggcaatg gatcgtttgg tgctgtcttt cagacgaaaa tgatgccaaag cggcgaggat 180
gctgccatta agagggtcct tcaagacaag cgcttcaaaa atcgagaact gcagattatg 240
cggattgttc gccatcctaa catcgtagaa ttgaaagcct tctattactc gaacggcgag 300
aggaaggatg aagtgtacct aaacctcggt ctcgaatacg taccagaaac cgtgtatcgg 360
gcgctgcggg actttaataa actcaaaacg actatgccaa tggttgaagt caagctgtat 420
atctatcaat tggtccgttc cctggcatac atccattcac aaggcatctg ccaccgtgac 480
atcaagcccc agaattctct acttgatcca tccaccggca tccataactc ctgcgacttt 540
ggttcggcca agattctggg agagaatgag cccaacgttt cctatatctg ttcccgtac 600
tatcgtgcgc cggaattgat ctttggcgcc actaattaca caacaaagat cgacgtgtgg 660
tccacggggt gtgtgatggc tgaactcatg cttggtcagc cattgttccc tggagagtcg 720
ggaattgacc aactggtgga aatcatcaag gttcttgga cccctactcg ggagcagatc 780
cgcaccatga acccaaaacta tatggagcac aaattccctc aaatcaagcc acaccattc 840
aacaagggtt tccggagagc tctcacgag gccattgatc tgatctcagc tttgctagaa 900
tacacgccga cacaacgtct ctccgctatc gaggcgatgt gccaccggtt cttcgacgaa 960
ctcagagatc ccaatacgcg actgcccgcg tctcggcacc ctggtggcgc tgctagagac 1020
ctccccaatc tctttgattt ctccagacat gaactttcta ttgcacctgc attgaacagc 1080
cggctgggtc cccctcatgc acgcgcgct ctcaggccc gggggctaga cattgacaac 1140
ttcactctc tcacgaagga ggagatgatg gcacgtctcg ac 1182

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<210> 42

<211> 394

<212> PRT

<213> *Aspergillus fumigatus*

<400> 42

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Met Ser Gln Asn Arg Pro Gly Val Phe Ser Asn Leu Arg Met Gly Glu
  1                      5                      10                      15

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Val Val Arg Glu Lys Val Gln Asp Gly Leu Thr Gly Glu Thr Lys Glu
      20                      25                      30

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Ile Ser Tyr Ser Gln Cys Lys Ile Val Gly Asn Gly Ser Phe Gly Val
 35 40 45
 Val Phe Gln Thr Lys Met Met Pro Ser Gly Glu Asp Ala Ala Ile Lys
 50 55 60
 Arg Val Leu Gln Asp Lys Arg Phe Lys Asn Arg Glu Leu Gln Ile Met
 65 70 75 80
 Arg Ile Val Arg His Pro Asn Ile Val Glu Leu Lys Ala Phe Tyr Tyr
 85 90 95
 Ser Asn Gly Glu Arg Lys Asp Glu Val Tyr Leu Asn Leu Val Leu Glu
 100 105 110
 Tyr Val Pro Glu Thr Val Tyr Arg Ala Ser Arg Tyr Phe Asn Lys Leu
 115 120 125
 Lys Thr Thr Met Pro Met Leu Glu Val Lys Leu Tyr Ile Tyr Gln Leu
 130 135 140
 Phe Arg Ser Leu Ala Tyr Ile His Ser Gln Gly Ile Cys His Arg Asp
 145 150 155 160
 Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Ser Thr Gly Ile Leu Lys
 165 170 175
 Leu Cys Asp Phe Gly Ser Ala Lys Ile Leu Val Glu Asn Glu Pro Asn
 180 185 190
 Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala Pro Glu Leu Ile Phe
 195 200 205
 Gly Ala Thr Asn Tyr Thr Thr Lys Ile Asp Val Trp Ser Thr Gly Cys
 210 215 220
 Val Met Ala Glu Leu Met Leu Gly Gln Pro Leu Phe Pro Gly Glu Ser
 225 230 235 240
 Gly Ile Asp Gln Leu Val Glu Ile Ile Lys Val Leu Gly Thr Pro Thr
 245 250 255
 Arg Glu Gln Ile Arg Thr Met Asn Pro Asn Tyr Met Glu His Lys Phe
 260 265 270
 Pro Gln Ile Lys Pro His Pro Phe Asn Lys Val Phe Arg Arg Ala Pro
 275 280 285
 His Glu Ala Ile Asp Leu Ile Ser Ala Leu Leu Glu Tyr Thr Pro Thr
 290 295 300
 Gln Arg Leu Ser Ala Ile Glu Ala Met Cys His Pro Phe Phe Asp Glu
 305 310 315 320
 Leu Arg Asp Pro Asn Thr Arg Leu Pro Asp Ser Arg His Pro Gly Gly
 325 330 335
 Ala Ala Arg Asp Leu Pro Asn Leu Phe Asp Phe Ser Arg His Glu Leu
 340 345 350
 Ser Ile Ala Pro Ala Leu Asn Ser Arg Leu Val Pro Pro His Ala Arg

355

360

365

Ala Ala Leu Glu Ala Arg Gly Leu Asp Ile Asp Asn Phe Thr Pro Leu
 370 375 380

Thr Lys Glu Glu Met Met Ala Arg Leu Asp
 385 390

<210> 43

<211> 2209

<212> DNA

<213> *Aspergillus fumigatus*

<400> 43

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<210> 44

<211> 2209

<212> DNA

<213> *Aspergillus fumigatus*

<400> 44

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aaccacccct caggacagca atcccagcag atccgctccg aggaggatga ccgttccatt 660
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<210> 45

<211> 735

<212> PRT

<213> *Aspergillus fumigatus*

<400> 45

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Pro Arg Gln Ser Thr Ala Phe Leu His Leu Thr Thr Tyr Asn Leu Arg
20 25 30

Gln His Gly Asn Trp Leu Tyr Leu Phe Glu Ser Val Thr Ser Gly Cys
35 40 45

Phe Ile Lys Ser Met Trp Lys Ser Phe Lys Glu Lys His Ala Ser Lys
50 55 60

Phe Gly Gly Gly Ser Ala Glu Ala Ala Ala Ser Asp Gly Gly Gln Asp
65 70 75 80

Leu Thr Thr Ile Leu Asp Arg Ser Gln Arg Gly Glu Leu Thr Val Leu

41/169

Glu Ala Ala His Gln Asp His Arg Leu Arg Val Thr Ile Gly Val Thr
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 Gly Ala Glu Ser Glu Val Phe Gly Leu Arg Trp Glu Thr Glu Pro Leu
 450 455 460
 Met Asn Leu Gly Asn Ala Leu Asp Leu Leu Val Thr Ser Ala Ala Trp
 465 470 475 480
 Thr Ala Gly Glu Gln Val Leu Lys Lys Thr Phe Leu Ser Gln Leu Leu
 485 490 495
 Thr Ala Val Ala Leu Pro Leu Gly Leu Leu Lys Val Ala Arg Val Val
 500 505 510
 Asp Asn Pro Phe Ser Val Ala Lys Ala Arg Ala Asp Lys Ala Gly Glu
 515 520 525
 Val Leu Ala Asp Ala Leu Ile Ser Lys Val Gln Gly Glu Arg Pro Val
 530 535 540
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 545 550 555 560
 Gln Ser Leu Ala Lys Arg Arg Ala Phe Gly Leu Val Glu Ser Ala Ile
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 Leu Met Gly Ala Pro Thr Pro Ser Asn Ser Glu Gln Trp Cys Arg Ile
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 Arg Ser Val Val Ser Gly Arg Leu Val Asn Val Tyr Ser Glu Asn Asp
 595 600 605
 Ser Val Leu Ala Leu Leu Tyr Arg Thr Ser Ser Leu Gln Leu Gly Val
 610 615 620
 Ala Gly Leu Gln Pro Val Glu Gly Val Ser Gly Val Glu Asn Leu Asp
 625 630 635 640
 Val Ser Asp Leu Ile Ser Gly His Leu Arg Tyr Gln Phe Leu Val Gly
 645 650 655
 Arg Ile Leu Ser Val Val Gly Leu Glu Ser Ile Asp Ala Arg Glu Val
 660 665 670
 Ala Leu Glu Glu Ala Ala Leu Glu Ala Lys Asp Arg Arg Gln Glu Gln
 675 680 685
 Glu Arg Ala His Asn Glu Arg Gln Ala Gly Phe Met Gly Glu Gly Arg
 690 695 700
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 <211> 510
 <212> DNA
 <213> *Aspergillus fumigatus*

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<210> 47
 <211> 423
 <212> DNA
 <213> *Aspergillus fumigatus*

<400> 47
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 aagcgtgtcc tggttgacgg tccttccacc gaggagaaca agatcggttc ccgtcacgct 180
 cttcctctcg ctcacgccac tctcaccctt ttcgtcattc ccaaactccc ccgcgctgcc 240
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<210> 48
 <211> 141
 <212> PRT
 <213> *Aspergillus fumigatus*

<400> 48
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 20 25 30
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 35 40 45
 Ser Thr Glu Glu Asn Lys Ile Val Pro Arg His Ala Leu Pro Leu Ala
 50 55 60
 His Ala Thr Leu Thr Pro Phe Val Ile Pro Lys Leu Pro Arg Ala Ala
 65 70 75 80
 Gly Thr Gly Pro Val Lys Lys Leu Trp Glu Lys Asn Glu Ile Asp Gly
 85 90 95
 Lys Trp Ala Lys Ser Thr Ile Ala Gln Lys Thr Glu Arg Ala Glu Arg
 100 105 110

Arg Lys Asn Leu Thr Asp Phe Glu Arg Phe Lys Val Leu Arg Leu Lys
 115 120 125

Lys Gln Val Arg Ser Val Cys Glu Thr Met Gly Glu Leu
 130 135 140

<210> 49

<211> 1413

<212> DNA

<213> *Aspergillus fumigatus*

<400> 49

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gcaacagcag ttcccccggt cactcaaaat gcggctgggt ccaaaggccc cacggcaatg 180
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<210> 50

<211> 1284

<212> DNA

<213> *Aspergillus fumigatus*

<400> 50

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<210> 51

<211> 428

<212> PRT

<213> *Aspergillus fumigatus*

<400> 51

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      20              25              30

Gly Gln Glu Gln Arg Lys Gly Leu Ala Thr Ala Val Pro Pro Val Thr
      35              40              45

Gln Asn Ala Ala Gly Ser Lys Gly Pro Thr Ala Met Val Phe Leu Asn
      50              55              60

Met Gly Gly Pro Ser Lys Ile Asp Glu Val Glu Asp Phe Leu Ser Arg
      65              70              75              80

Leu Phe Ala Asp Gly Asp Leu Ile Pro Leu Gly Arg Leu Gln Ser Tyr
      85              90              95

Leu Gly Pro Leu Ile Ala Lys Arg Arg Thr Pro Lys Ile Gln Arg Gln
      100             105             110

Tyr Ser Asp Ile Gly Gly Gly Ser Pro Ile Arg Lys Trp Ser Glu Tyr
      115             120             125

Gln Cys Glu Glu Met Cys Arg Leu Leu Asp Lys Ile Asn Pro Glu Thr
      130             135             140

Ala Pro His Lys Pro Tyr Val Ala Phe Arg Tyr Ala Asp Pro Leu Thr
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Glu Glu Met Tyr Thr Lys Leu Leu Glu Asp Gly Phe Gly Asn Gly Lys
      165             170             175

Gly Gly Arg Ala Val Ala Phe Thr Gln Tyr Pro Gln Tyr Ser Cys Ser
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Thr Thr Gly Ser Ser Leu Asn Glu Leu Trp Lys Trp Arg Thr Arg Leu
      195             200             205

Glu Gly Lys Arg Ala Asn Gly Asn Met Asp Pro Ala Gly Ala Ile Gln
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Trp Ser Val Ile Asp Arg Trp Pro Thr His Pro Gly Leu Val Glu Ala
      225             230             235             240

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 260 265 270
 Val Val Asn Arg Gly Asp Pro Tyr Pro Ala Glu Val Ala Ala Thr Val
 275 280 285
 His Ala Val Met Gln Arg Leu Asn Phe Ser Asn Pro Tyr Arg Leu Cys
 290 295 300
 Trp Gln Ser Gln Val Gly Pro Ser Ala Trp Leu Gly Ala Gln Thr Ser
 305 310 315 320
 Asp Thr Val Glu Asn Tyr Val Lys Arg Gly Gln Thr Asp Ile Ile Leu
 325 330 335
 Val Pro Ile Ala Phe Thr Ser Asp His Ile Glu Thr Leu Tyr Glu Leu
 340 345 350
 Asp Leu Glu Val Ile Lys Glu Ala Asn Ser Pro Gly Val Lys Arg Ala
 355 360 365
 Glu Ser Leu Asn Gly Asn Pro Ile Phe Ile Gln Ala Leu Ala Asp Ile
 370 375 380
 Ala Gln Glu His Leu Arg Lys Gly Glu Lys Cys Ser Leu Gln Met Thr
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<210> 52

<211> 1536

<212> DNA

<213> *Aspergillus fumigatus*

<400> 52

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 ttctcctcat ctccggtgcg ggctggcatt gccgatcatg aatcaactcc ctgcactgtc 180
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 accgctgcag caggccagac agcgaccact ggccacgaca gctggcgagg catgttgttc 1020

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agcaaggata gcatcggtgg ttggctcctg ggtggcattc tctttgcatg gcagtttcct 1080
catttcaatg ctttgtccta catgatccgt gaagagtaca aggcagccgg gtacaggatg 1140
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<210> 53

<211> 1536

<212> DNA

<213> *Aspergillus fumigatus*

<400> 53

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<210> 54

<211> 512

<212> PRT

<213> *Aspergillus fumigatus*

<400> 54

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Arg Pro Val Ala Val Arg Ser Phe Phe Ser Ser Ser Arg Leu Arg Ala
      35             40             45

Gly Ile Ala Asp His Glu Ser Thr Pro Ser Thr Val Gln Lys Thr Tyr

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Pro His Arg Arg Arg Lys Arg Leu Lys Glu Glu Ala Ala Lys Asn Asn		
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Ala Ala Glu Thr Glu Leu Pro Pro Asp Ala Ser Ser Gln Leu Ser Thr		
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Leu Ser Ser Ala Leu Pro Ala Thr Ser Leu Arg Arg Lys Leu Ala Ala		
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Phe Leu Ala Leu Thr Lys Pro Arg Leu Ser Phe Leu Ile Val Leu Thr		
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Asp Pro Ser Met Thr Pro Leu Pro Thr Leu Ser Thr Ser Thr Leu Thr		
	195	200 205
Phe Leu Tyr Leu Thr Thr Gly Thr Phe Leu Ser Ser Cys Ser Ala Asn		
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Thr Leu Asn Met Leu Leu Glu Pro Lys Tyr Asp Ala Leu Met Ser Arg		
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Thr Arg Asn Arg Pro Leu Val Arg Gly Leu Leu Ser Arg Arg Ala Ala		
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Val Leu Phe Ala Ile Ala Thr Ala Ala Ala Gly Leu Gly Leu Leu Tyr		
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Ile Gly Thr Asn Pro Thr Thr Thr Ala Leu Ser Ala Ser Asn Ile Cys		
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Leu Tyr Ala Phe Val Tyr Thr Pro Leu Lys Arg Ile Ser Val Ile Asn		
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Asp Met Leu Phe Ser Lys Asp Ser Ile Gly Gly Trp Leu Leu Gly Gly		
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	355	360 365
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	370	375 380

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 405 410 415
 Phe Leu Val Gly Ser Thr Ala Ala Asn Gly Trp Leu Val Lys Glu Ala
 420 425 430
 Tyr Lys Phe Trp Arg His Gln Gly Ala Asn Gly Ser Ala Arg Arg Leu
 435 440 445
 Phe Trp Ala Ser Ile Trp Gln Leu Pro Ile Leu Leu Val Gly Gly Leu
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 Val Thr Lys Lys Gly Leu Trp Asp Gly Val Trp Asn Asn Val Phe Gly
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 Val Ala Glu Ala Glu Arg Lys Met Ile Pro Ala Lys Thr Ser Ser Ser
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<210> 55

<211> 1626

<212> DNA

<213> *Aspergillus fumigatus*

<400> 55

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<210> 56

<211> 1626

<212> DNA

<213> *Aspergillus fumigatus*

<400> 56

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gctggctcatg atcaatcatc tcaaaaggcc tctccgtgt caaatgcaga gtcagagtcc 360
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<210> 57

<211> 542

<212> PRT

<213> *Aspergillus fumigatus*

<400> 57

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Ala Pro Leu Phe Ser Thr Ala Pro Phe Arg Arg Gln Leu His Ala Ser
      35             40             45

Gly Val Arg Ser Ile Glu Pro Val Ile Phe Arg Asn Ser Leu Glu Lys
      50             55             60

Thr Leu Glu Ala His Arg Ser Ser Asn Arg Ala Ser Leu Ile Arg Lys
      65             70             75             80

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Val Ile Asn His Asp Cys Pro Ala Glu Thr Pro Pro Pro Ile Leu Pro
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 115 120 125
 Arg Ala Gln Arg Lys Ala Arg Ser Pro Ser Gln Val Ala Thr Pro Gln
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 Pro Gln Thr Thr Glu Tyr Pro Gln Leu Gln Trp His Ala Asp Glu Thr
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 Lys Gly Arg Pro Ala Gln Ser Pro Trp Leu Lys Tyr Leu Thr Thr Asp
 165 170 175
 Trp Lys Thr Pro Asp Ala Val Ser Arg Leu Asp Ala Glu Ile Arg Ala
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 Leu Glu Leu Tyr Met Thr Pro Thr Pro Ser Glu Arg Thr Glu Ile Asp
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 Arg Leu Val Ala Asp Met Gly Arg Leu Leu Ala Gly Ile Val Pro Ser
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 Ser Gly Leu Asp Phe Val Leu Pro Val Pro Asp Ser Asp Arg Ser Thr
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 Arg Asp Val Arg Lys Pro Ser Ala Thr Arg Pro Lys Val Leu Gln Thr
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 Tyr Lys Lys Leu Leu His Glu Val Gly His Ala Leu Gln Gln Ser Pro
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 Ser Ala Ile His Arg Pro Thr Gly Arg Leu Leu Gln Phe His Cys Gly
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 Ala Arg Gly Arg Tyr Gly Arg Thr Gln Met Ser Ile Glu Ser Asp Ala
 355 360 365
 Leu Val Met Leu Leu Val Ala Phe Leu Lys Met Asn His Gly Arg Phe
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 Gln Arg Pro Asp Cys Leu Gly Glu Gln Leu Ile Ala Phe Leu Arg Ala
 385 390 395 400

Tyr Gly Ser Asp Ile Asp Leu Thr Thr Thr Gly Val Ser Val Asp Pro
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 Ser Leu Lys Arg Thr Ala Ala Ala Arg Arg Asn Leu Pro Ala Ala Ser
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 Arg Leu Cys Val Gln Asp Pro Thr Asn Tyr Met Asn Asp Leu Gly Arg
 465 470 475 480
 Ser Cys Val Arg Thr Leu Glu Leu Gln His Thr Phe Ser Leu Ala His
 485 490 495
 Asp Arg Leu Gly Ala Ser Leu Lys Arg Trp Asp Asp Ser Glu Pro Ala
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<210> 58

<211> 2356

<212> DNA

<213> *Aspergillus fumigatus*

<400> 58

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<210> 59

<211> 2356

<212> DNA

<213> *Aspergillus fumigatus*

<400> 59

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2356

<210> 60

<211> 785

<212> PRT

<213> Aspergillus fumigatus

<400> 60

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 35 40 45

Pro Val Val Asp Ala Met Glu Arg Thr Lys Asn Ala Ile Gln Ser Asn
 50 55 60

Asn Ser Ser Ser Arg Ala Gln Leu Ser Asp Ala Leu Pro Glu Ser Glu
 65 70 75 80

Lys Ser Gln Ser Ala Gly Gln Val Ile Val Pro Thr Arg Met Gln Glu
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Leu Leu Asp Arg Gly Arg Pro Ile Glu Ala Ala Gln Phe Phe Leu Glu
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Thr His Ala Ala Ser Leu Lys Gly Ile Ser Ser Asp Arg Lys Glu Met
 115 120 125

Ala Thr Lys Val Phe Phe Val Asn Cys Lys Glu Asp Asn Val Phe Ile
 130 135 140

Ala Arg Ser Val Phe Glu Arg Leu Glu Glu Val Asp Arg Ile Thr Pro
 145 150 155 160

Glu Met Trp Lys Thr Leu Met Leu Ala Leu Ala Lys Lys Gly Cys Ile
 165 170 175

Glu Ser Val Ala Ser Val Tyr Thr Arg Tyr Met Arg Lys Phe Pro Cys
 180 185 190

Pro Pro Glu Met Val Asp Val Val Leu Arg Ser Leu Leu Glu Ser His
 195 200 205

Arg Leu Thr Thr Ala Lys Trp Phe Leu Leu Arg Asn Leu Gln His Asp
 210 215 220

Arg Asp Cys Gly Leu Cys Gly Ala Tyr Leu Ser Gly Leu Trp Arg Lys
 225 230 235 240

Thr Arg Ser Ile Glu Leu Leu Asn Gly Gln Leu Lys Lys Ile Leu Thr
 245 250 255

Ile Leu Pro Lys Phe Glu Lys Gln Pro Ser Asp Lys Leu Phe Asn Pro
 260 265 270

Val Ile Lys Ala Tyr Val Glu Phe Gly Arg Val Ala Asp Ala Glu Ala

275					280					285					
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Arg	Arg	Arg	Asp	Phe	Leu	Pro	Ile	Phe	Asp	Arg	Ile	Phe	Leu	Glu	Tyr
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		355					360					365			
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370						375				380					
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Gln	Phe	Leu	Glu	Ile	Leu	Arg	Ser	Arg	Arg	Leu	Ala	Leu	Glu	Gly	Ala
			420					425					430		
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His	Ser	Ser	Thr	Ser	Gln	Arg	Ile	Met	Gly	Tyr	Asp	Gln	Gln	Ser	Phe
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Gln	Tyr	Gln	Lys	Leu	His	Lys	Gln	Met	Thr	His	Phe	Leu	His	Ala	Gly
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Lys	Leu	Lys	Glu	Ala	Leu	Lys	Cys	Phe	Gln	Asn	Ala	Lys	Asn	Ala	Arg
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Phe	Gln	Met	Arg	Gln	Leu	His	Val	Glu	Leu	Ala	Val	Ile	Ala	Thr	Leu
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Leu	Glu	Asp	Gly	Leu	Ser	Ala	Ala	Arg	Ser	Leu	Ile	Glu	Ser	Glu	Trp
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Arg	Thr	Ile	Arg	His	Leu	Val	Arg	Phe	Ser	Pro	Ile	Phe	Phe	Arg	Gln
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Val	Met	Ala	Val	Asp	Glu	Asp	Ala	Gly	Gly	His	Ile	Val	Gln	Met	Ala
			580					585					590		
Val	Leu	Arg	Phe	Tyr	Gln	Leu	Cys	Trp	Ser	Thr	Lys	His	Met	Lys	Val
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Lys His His Leu Thr Val Ala Thr Ser Arg Arg Leu Ile Ser Gln His
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 Lys Pro Glu Met Ala Leu Glu Leu Leu Thr Ala Val Tyr Lys Ser Arg
 625 630 635 640
 Tyr Arg Phe Ala Ala Thr Phe Asp Gly Val Cys Met Lys Met Phe Ala
 645 650 655
 Arg Ala Phe Ala Ala Thr Asp Asn Ile Leu Gly Leu Arg Trp Cys Ile
 660 665 670
 Leu Thr Ala Leu Ser Arg Asp Ser Ala Leu Asn His Asp Phe Val Val
 675 680 685
 Glu Val Arg Arg Ile Leu Gly Thr Leu Ser Pro Pro Ser Ala Val Asp
 690 695 700
 Ala Thr Ala Gly Pro Val Thr His Glu Gln Leu Glu Tyr Leu Tyr Tyr
 705 710 715 720
 Ile Ala Asp Leu Leu Glu Glu Lys Asn Glu Gly Cys Ala Pro Ile Trp
 725 730 735
 Glu Leu Lys His Asp Ala Thr Leu Lys Gln Ser Ser Arg Arg Gln Leu
 740 745 750
 Lys Gln Pro Leu Asp Ala Ser Arg Leu Phe Asn Gln Ser Asp Val Arg
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 770 775 780
 Gly
 785

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 <213> Artificial sequence

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 <223> PCR primer Impl

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21

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19

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20

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<223> PCR primer ppyr3

<400> 64
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21

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<223> (21)..(30)
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35

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<220>
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<220>
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21

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<210> 74
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<210> 77
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<400> 77
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<220>
<223> PCR primer 2.1.1.5

<400> 79
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<210> 80
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tccagtcaag gttggtgatg 20

<210> 81
<211> 19

<212> DNA
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<220>
<223> PCR primer 2.1.1.9

<400> 81
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19

<210> 82
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<223> PCR primer 4.3.4.2

<400> 82
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<210> 83
<211> 20
<212> DNA
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<220>
<223> PCR primer 5.3.11.2

<400> 83
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20

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<400> 84
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21

<210> 85
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<400> 85
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20

<210> 86
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<213> Artificial sequence

<220>

<223> PCR primer 7.5.9.4

<400> 86

accaggagaa tcagcgacac

20

<210> 87

<211> 20

<212> DNA

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<220>

<223> PCR primer 8.62.2

<400> 87

gggacgaaga atacgagctg

20

<210> 88

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<212> DNA

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<223> PCR primer Gt11f1

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19

<210> 89

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<223> PCR primer Gt11f3

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gcacattggc tgaatatcg

19

<210> 90

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<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer Gt11Rev

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ttgacaccag accaactggt aatg

24

<210> 91

<211> 3052

<212> DNA

<213> Aspergillus fumigatus

<220>

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 91

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<210> 92

<211> 2052

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
Genomic sequence containing the coding region

<400> 92

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<210> 93

<211> 2052

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
Coding region without introns

<400> 93

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ctgccccaat	ctacagatgc	acaagaagac	cagtcatact	ccggcagcgc	agcgaacggt	300
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<210> 94

<211> 683

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
Protein sequence

<400> 94

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Ala Ala Asn Gly Ser Arg Thr Asp Pro Gln Phe Lys Asp Pro Glu Thr

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<211> 3814

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466
 Genomic sequence containing 3' and 5'-ends and the coding region

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<210> 96

<211> 2814

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466
 Genomic sequence containing the coding region

<400> 96

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<210> 97

<211> 2814

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466

Coding region without introns

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<210> 98
 <211> 937
 <212> PRT
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466
 Protein sequence

<400> 98

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Ser	Phe	Cys	Thr	Val	Ala	Ala	Ile	Thr	Tyr	Asp	Val	His	Arg	Arg	Val	35	40	45	
Arg	Val	Ala	Glu	Arg	Ile	Val	Glu	Asn	Lys	Arg	Ala	Leu	Gln	Thr	Ser	50	55	60	
Ala	Pro	Asn	Tyr	Asp	Ala	Thr	Ser	Ala	Ala	Lys	Arg	Leu	Ala	Arg	Met	65	70	75	80
Met	Glu	Ala	Ala	Glu	Ala	Gly	Glu	Phe	Met	Gly	Leu	Ala	Ser	Leu	Lys	85	90	95	
Glu	Ala	Asp	Arg	Lys	Ile	Arg	Glu	Gly	Gln	Ala	Thr	Gln	Asp	Asp	Asp	100	105	110	
Val	Val	Ala	Leu	His	Gln	Glu	Gly	Gly	Phe	Arg	Arg	Pro	Gly	Met	Gly	115	120	125	
Leu	Glu	Asp	Pro	Arg	Arg	Ala	Val	Gln	Ala	Glu	Ser	Tyr	Leu	Glu	Thr	130	135	140	
Thr	Arg	Ser	Gln	Leu	Val	Asp	Ala	Leu	Ile	Ser	Arg	Pro	Asn	Leu	Glu	145	150	155	160
Ser	Gly	Leu	Gly	Arg	Arg	Asn	Phe	Val	Pro	Pro	Arg	Gln	Val	Pro	Val	165	170	175	
Val	Asp	Ala	Met	Glu	Arg	Thr	Lys	Asn	Ala	Ile	Gln	Ser	Asn	Asn	Ser	180	185	190	
Ser	Ser	Arg	Ala	Gln	Leu	Ser	Asp	Ala	Leu	Pro	Glu	Ser	Glu	Lys	Ser	195	200	205	
Gln	Ser	Ala	Gly	Gln	Val	Ile	Val	Pro	Thr	Arg	Met	Gln	Glu	Leu	Leu	210	215	220	
Asp	Arg	Gly	Arg	Pro	Ile	Glu	Ala	Ala	Gln	Phe	Phe	Leu	Glu	Thr	His	225	230	235	240
Ala	Ala	Ser	Leu	Lys	Gly	Ile	Ser	Ser	Asp	Arg	Lys	Glu	Met	Ala	Thr	245	250	255	
Lys	Val	Phe	Phe	Val	Asn	Cys	Lys	Glu	Asp	Asn	Val	Phe	Ile	Ala	Arg	260	265	270	

Ser Val Phe Glu Arg Leu Glu Glu Val Asp Arg Ile Thr Pro Glu Met
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 Trp Lys Thr Leu Met Leu Ala Leu Ala Lys Lys Gly Cys Ile Glu Ser
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 305 310 315 320
 Glu Met Val Asp Val Val Leu Arg Ser Leu Leu Glu Ser His Arg Leu
 325 330 335
 Thr Thr Ala Lys Trp Phe Leu Leu Arg Asn Leu Gln His Asp Arg Asp
 340 345 350
 Cys Gly Leu Cys Gly Ala Tyr Leu Ser Gly Leu Trp Arg Lys Thr Arg
 355 360 365
 Ser Ile Glu Leu Leu Asn Gly Gln Leu Lys Lys Ile Leu Thr Ile Leu
 370 375 380
 Pro Lys Phe Glu Lys Gln Pro Ser Asp Lys Leu Phe Asn Pro Val Ile
 385 390 395 400
 Lys Ala Tyr Val Glu Phe Gly Arg Val Ala Asp Ala Glu Ala Leu Val
 405 410 415
 His Asp Met Thr Thr Leu Tyr Gly Ile Pro Leu Arg Cys Arg Thr Gln
 420 425 430
 Gly Leu Leu Val Tyr Ala Lys Ala Leu Asn Cys Asp Trp Glu Gly Val
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 Asp Ala Gly Leu Gln Glu Met His Lys Leu Lys Leu Thr Arg Arg Arg
 450 455 460
 Arg Asp Phe Leu Pro Ile Phe Asp Arg Ile Phe Leu Glu Tyr Trp Val
 465 470 475 480
 Ser His Ser Gly Ile Glu Ile Arg Asn Phe Val Phe Arg Tyr Leu Asp
 485 490 495
 Lys Phe Asp Ile Val Pro Asp Arg Val Leu Tyr Lys His Ile Leu Glu
 500 505 510
 Ala Phe Val Glu Lys Gly Asp Lys Glu Met Ile Ala Glu Phe Thr Ser
 515 520 525
 Met Ala Lys Gln Arg Ser Trp Asn Ile Pro Ile Asn Glu Gln Gln Phe
 530 535 540
 Leu Glu Ile Leu Arg Ser Arg Arg Leu Ala Leu Glu Gly Ala Pro Val
 545 550 555 560
 Gly Phe Trp Gln Met Leu Gln Ala Ala Arg Val Lys Tyr Gly His Ser
 565 570 575
 Ser Thr Ser Gln Arg Ile Met Gly Tyr Asp Gln Gln Ser Phe Pro Leu
 580 585 590

Pro Glu Val Asn Ser Met Pro Tyr Thr Gln Asn Pro Leu Ser Trp Tyr
 595 600 605
 Gln Arg Thr Met Gln Glu Thr Thr Pro Ser Lys Pro Val Asp Gln Tyr
 610 615 620
 Gln Lys Leu His Lys Gln Met Thr His Phe Leu His Ala Gly Lys Leu
 625 630 635 640
 Lys Glu Ala Leu Lys Cys Phe Gln Asn Ala Lys Asn Ala Arg Phe Gln
 645 650 655
 Met Arg Gln Leu His Val Glu Leu Ala Val Ile Ala Thr Leu Leu Glu
 660 665 670
 Asp Gly Leu Ser Ala Ala Arg Ser Leu Ile Glu Ser Glu Trp Arg Thr
 675 680 685
 Ile Arg His Leu Val Arg Phe Ser Pro Ile Phe Phe Arg Gln Val Met
 690 695 700
 Ala Val Asp Glu Asp Ala Gly Gly His Ile Val Gln Met Ala Val Leu
 705 710 715 720
 Arg Phe Tyr Gln Leu Cys Trp Ser Thr Lys His Met Lys Val Lys His
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 His Leu Thr Val Ala Thr Ser Arg Arg Leu Ile Ser Gln His Lys Pro
 740 745 750
 Glu Met Ala Leu Glu Leu Leu Thr Ala Val Tyr Lys Ser Arg Tyr Arg
 755 760 765
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 805 810 815
 Arg Arg Ile Leu Gly Thr Leu Ser Pro Pro Ser Ala Val Asp Ala Thr
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 Ala Gly Pro Val Thr His Glu Gln Leu Glu Tyr Leu Tyr Tyr Ile Ala
 835 840 845
 Asp Leu Leu Glu Glu Lys Asn Glu Gly Cys Ala Pro Ile Trp Glu Leu
 850 855 860
 Lys His Asp Ala Thr Leu Lys Gln Ser Ser Arg Arg Gln Leu Lys Gln
 865 870 875 880
 Pro Leu Asp Ala Ser Arg Leu Phe Asn Gln Ser Asp Val Arg Glu Thr
 885 890 895
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915

920

925

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<210> 99

<211> 2401

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 99

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tgggttgggt tgctctgctt ataattctct cggcattgct gtaatcaatc cacttttctc      240
tggggccctt ctacacatgc agcaatttca ttggtcatct gagatataca gatttgtaag      300
gcagtatcag tatcatcagg atacgcttct atgtagtatg agctcaaaga acagatagtt      360
gagaagtagt actgatatac cgtggtttaa gtattttgtc ggagtgtctaa gcattacaag      420
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<210> 100

<211> 1401

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
Genomic sequence containing the coding region

<400> 100

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gtgccacaag	acgcctccca	gctacgaaat	tggagaaaag	agacatttgc	aacactcatt	360
gccgttggtt	tagaccgaa	tcgctcaacg	attttctacc	agtccgccgt	atgcagtatg	420
aatatgggtt	gtaaagttta	ctgaccatgt	cattaggtcc	atgcacacgc	cgaactattt	480
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cgggttatgt	ccctcaaaga	accgacgttg	aaaatgtcca	agtcccatgc	cgacagacgc	1020
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<210> 101

<211> 1200

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
Coding region without introns

<400> 101

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tcagagacgg	cgaaatcatc	ttcagctgca	aatcagacca	tattctctgg	gatccagcca	180
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gtgccacaag	acgcctccca	gctacgaaat	tggagaaaag	agacatttgc	aacactcatt	360
gccgttggtt	tagaccgaa	tcgctcaacg	attttctacc	agtccgccgt	ccatgcacac	420
gccgaactat	tttggatttt	gtgcacaata	gcctctatgg	gatatctctc	ccgaatgaca	480
cagtggaga	aggaacagct	agctgacgtc	ggccagagca	aactccagtt	gcctgataac	540
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tcgcccgcag	aaatctccaa	aaagatcaat	gctgcgctca	cagactcgga	attaaccatt	900
acatatgacc	cagtcgctcg	acctggagtg	gcgaatttaa	tagagatctt	gagtcacttc	960
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tcacttgtag gagatcagac tgactacctt gattctatag cagaacaggg ttctgaagcc 1140
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<210> 102

<211> 399

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
Protein sequence

<400> 102

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Glu Val Phe Arg Arg Trp Ser Ser Ser Glu Thr Ala Lys Ser Ser Ser
              35              40              45

Ala Ala Asn Gln Thr Ile Phe Ser Gly Ile Gln Pro Thr Gly Val Pro
              50              55              60

His Leu Gly Asn Tyr Leu Gly Ala Leu Arg Glu Trp Val Arg Leu Gln
65              70              75              80

Asn Ala Ala Lys Glu Gly Thr Arg Leu Phe Phe Ser Ile Val Asp Leu
              85              90              95

His Ala Leu Thr Val Pro Gln Asp Ala Ser Gln Leu Arg Asn Trp Arg
              100             105             110

Lys Glu Thr Phe Ala Thr Leu Ile Ala Val Gly Leu Asp Pro Asn Arg
              115             120             125

Ser Thr Ile Phe Tyr Gln Ser Ala Val His Ala His Ala Glu Leu Phe
              130             135             140

Trp Ile Leu Cys Thr Ile Ala Ser Met Gly Tyr Leu Ser Arg Met Thr
145             150             155             160

Gln Trp Lys Lys Glu Gln Leu Ala Asp Val Gly Gln Ser Lys Leu Gln
              165             170             175

Leu Pro Asp Asn Ala Asn Leu Glu Asp Ser Thr Ala Arg Ser Arg Leu
              180             185             190

Arg Leu Gly Leu Phe Ser Tyr Pro Val Leu Gln Ala Ala Asp Ile Leu
              195             200             205

Ile Arg Ala Thr His Val Pro Val Gly Asp Asp Gln Arg Gln His Leu
              210             215             220

Glu Phe Ser Arg Asn Thr Ala Asn Ser Phe Asn His Val Tyr Gly Pro
225             230             235             240

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Ile Phe Pro Ser Pro Glu Ala Ile Ile Ser Pro Ala Lys Arg Val Met
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Ser Leu Lys Glu Pro Thr Leu Lys Met Ser Lys Ser His Ala Asp Arg
 260 265 270

Arg Ser Arg Ile Ile Leu Thr Asp Ser Pro Ala Glu Ile Ser Lys Lys
 275 280 285

Ile Asn Ala Ala Leu Thr Asp Ser Glu Leu Thr Ile Thr Tyr Asp Pro
 290 295 300

Val Arg Arg Pro Gly Val Ala Asn Leu Ile Glu Ile Leu Ser His Phe
 305 310 315 320

Asp Gly Arg Thr Cys Asp Glu Ile Ala Met Glu Tyr Arg Ser Ala Ser
 325 330 335

Leu Arg Ala Leu Lys Glu His Leu Ala Arg Thr Leu Ser Asn His Leu
 340 345 350

Glu Pro Ile Arg Glu Lys Tyr Leu Ser Leu Val Gly Asp Gln Thr Asp
 355 360 365

Tyr Leu Asp Ser Ile Ala Glu Gln Gly Ser Glu Ala Ala Arg Ala Asn
 370 375 380

Ala Glu Leu Thr Met Glu Gln Val Lys Val Ala Met Gly Leu Ile
 385 390 395

<210> 103

<211> 3805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 103

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acagagtttg	ttagctcacc	gcctttggat	tttactgct	aaaacaaaaa	aaaagtgaga	240
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cacggactgg	ttcaggaaaag	acggccgctt	tcgttatccc	aatgatcgag	aaattgaaga	960
gccatagcac	caagggttga	gcccgcggtc	tggtcttgtc	cccacgcaga	gagctggcac	1020
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<210> 104

<211> 2805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
Genomic sequence containing the coding region

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<210> 105

<211> 2805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350

Coding region without introns

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<210> 106

<211> 934

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350
Protein sequence

<400> 106

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 145 150 155 160
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 165 170 175
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 Lys Val Glu Met Asn Leu Asp Leu Ser Ser Ile Arg Tyr Val Val Phe
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 465 470 475 480
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 Val Val Thr Gly Ser Leu Pro Arg Asp Gly Leu Ser Gln Ser Cys Glu
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 Pro Glu Thr Ile Phe Glu Val Asn Asn Arg Arg Met Gly Lys His Glu
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 645 650 655
 Asp Gly Pro Asp Asp Gly Lys Ala Val Asn Glu Ala Lys Glu Thr Glu
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	740	745 750
Ser Asn Phe Ala Gln	Ala Ser Arg Ser Ala	Thr Met Asp Leu Ala Gly
	755	760 765
Asp Asp Gly Gly Arg	Gly Phe Gly Glu Ala	Arg Thr Leu Met Arg Trp
	770	775 780
Asp Lys Arg His Lys	Lys Tyr Val Ala Arg	Gln Asn Asp Glu Asp Gly
	785	790 795 800
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<210> 107

<211> 2413

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
 Genomic sequence containing 3' and 5'-ends and the coding region

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<210> 108

<211> 1413

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
Genomic sequence containing the coding region

<400> 108

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<210> 109

<211> 1287

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
Coding region without introns

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<210> 110

<211> 428

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420
Protein sequence

<400> 110

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 Gly Gln Glu Gln Arg Lys Gly Leu Ala Thr Ala Val Pro Pro Val Thr
 35 40 45
 Gln Asn Ala Ala Gly Ser Lys Gly Pro Thr Ala Met Val Phe Leu Asn
 50 55 60
 Met Gly Gly Pro Ser Lys Ile Asp Glu Val Glu Asp Phe Leu Ser Arg
 65 70 75 80
 Leu Phe Ala Asp Gly Asp Leu Ile Pro Leu Gly Arg Leu Gln Ser Tyr
 85 90 95
 Leu Gly Pro Leu Ile Ala Lys Arg Arg Thr Pro Lys Ile Gln Arg Gln
 100 105 110
 Tyr Ser Asp Ile Gly Gly Gly Ser Pro Ile Arg Lys Trp Ser Glu Tyr
 115 120 125
 Gln Cys Glu Glu Met Cys Arg Leu Leu Asp Lys Ile Asn Pro Glu Thr
 130 135 140
 Ala Pro His Lys Pro Tyr Val Ala Phe Arg Tyr Ala Asp Pro Leu Thr
 145 150 155 160
 Glu Glu Met Tyr Thr Lys Leu Leu Glu Asp Gly Phe Gly Asn Gly Lys
 165 170 175
 Gly Gly Arg Ala Val Ala Phe Thr Gln Tyr Pro Gln Tyr Ser Cys Ser
 180 185 190
 Thr Thr Gly Ser Ser Leu Asn Glu Leu Trp Lys Trp Arg Thr Arg Leu
 195 200 205
 Glu Gly Lys Arg Ala Asn Gly Asn Met Asp Pro Ala Gly Ala Ile Gln
 210 215 220
 Trp Ser Val Ile Asp Arg Trp Pro Thr His Pro Gly Leu Val Glu Ala
 225 230 235 240
 Phe Ala Arg Asn Ile Glu Glu Gln Leu Lys Thr Tyr Pro Glu Glu Lys
 245 250 255
 Arg Asn Gly Val Val Leu Leu Phe Ser Ala His Ser Leu Pro Met Ser
 260 265 270
 Val Val Asn Arg Gly Asp Pro Tyr Pro Ala Glu Val Ala Ala Thr Val
 275 280 285
 His Ala Val Met Gln Arg Leu Asn Phe Ser Asn Pro Tyr Arg Leu Cys
 290 295 300
 Trp Gln Ser Gln Val Gly Pro Ser Ala Trp Leu Gly Ala Gln Thr Ser
 305 310 315 320
 Asp Thr Val Glu Asn Tyr Val Lys Arg Gly Gln Thr Asp Ile Ile Leu
 325 330 335

Val Pro Ile Ala Phe Thr Ser Asp His Ile Glu Thr Leu Tyr Glu Leu
 340 345 350

Asp Leu Glu Val Ile Lys Glu Ala Asn Ser Pro Gly Val Lys Arg Ala
 355 360 365

Glu Ser Leu Asn Gly Asn Pro Ile Phe Ile Gln Ala Leu Ala Asp Ile
 370 375 380

Ala Gln Glu His Leu Arg Lys Gly Glu Lys Cys Ser Leu Gln Met Thr
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Leu Arg Cys Gln Gly Cys Lys Ser Glu Arg Cys Leu Glu Gln Lys Lys
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<210> 111

<211> 2865

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 111

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<210> 112

<211> 1865

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
Genomic sequence containing the coding region

<400> 112

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<210> 113
 <211> 1725
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
 Coding region without introns

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tattatggct tcaggaatat aaaaaatctc gtcagaaaac ttaaaccgcg acgcgtgtca     1200
agactgccag gcgccaagcc gcaagcggtc tcttcaagtg caaatcgacg acagcccatg     1260
tcaaggaacg cagctccggc tggaacaggc gctgattatg catatgttga agtcatggct     1320
tgtcctggcg gctgtacca tgggtgggtgg caaataagga ttgaagatgc ccgggagggt     1380
gttccgaacg cactaaaaga gacatcgact gaaactcctg tggctgcacc gaaaccacg     1440
ccgcatgagc agcgtgcctg gctagcccg gtagatgaag cgtactactc tgcggactcg     1500
gatagcgagg gatctgtcac gacggagccg gtttctgtcc tgtcaaggga taaccagatt     1560
catgagtttt tgaactattg gtcagagaag gttgatatac ccctttcccg gctcgcgtac     1620
acgtcctatc gcgaagtgga gagcgacgtg ggtaagacga agaatgcgcc caacgaaact     1680
gctcgtgttg tggaattggc aggaaagatc ggaggtggtt ggtga                        1725

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<210> 114
 <211> 574
 <212> PRT
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
 Protein sequence

<400> 114

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Met Ser Ala Ile Leu Ser Ala Asp Asp Leu Asn Asp Phe Ile Ser Pro
1           5           10           15

Gly Val Ala Cys Ile Lys Pro Val Glu Ser Leu Pro Gln Lys Glu Ser
20          25          30

Gln Ser Glu Asn Pro Tyr Glu Val Thr Lys Glu Asp Lys Val Gln Pro
35          40          45

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Glu Asn Leu Pro Pro Ala Gln Ile Ser Leu Thr Asp Cys Leu Ala Cys
 50 55 60
 Ser Gly Cys Val Thr Ser Ala Glu Ala Val Leu Ile Ser Leu Gln Ser
 65 70 75 80
 His Thr Glu Val Leu Asn Thr Leu Asp Ser Asp Gly Arg Ile Phe Val
 85 90 95
 Ala Ser Val Ser Pro Gln Val Arg Ala Ser Leu Ala Ala Thr Tyr Gly
 100 105 110
 Ile Thr Glu Arg Glu Ala Lys Tyr Met Ile Asp Gln Phe Leu Met Gly
 115 120 125
 Pro His Gly Leu Arg Ala Gly Gly Lys His Gly Asn Gly Phe Thr Trp
 130 135 140
 Val Val Asp Thr Asn Val Met Arg Glu Ala Val Leu Ala Leu Thr Ala
 145 150 155 160
 Asp Glu Val Thr Ser Ser Leu Leu Ser Thr Gly Ser Gly Ser Leu Pro
 165 170 175
 Lys Ser Pro Ile Leu Ser Ser Ala Cys Pro Gly Trp Ile Cys Tyr Ala
 180 185 190
 Glu Lys Thr His Pro Phe Ile Leu Pro His Leu Ser Arg Leu Lys Ser
 195 200 205
 Pro Gln Ala Leu Ser Gly Thr Phe Leu Lys Ser Val Leu Ser Lys Ala
 210 215 220
 Leu Gly Val Pro Pro Ser Gln Ile Trp His Leu Ala Ile Met Pro Cys
 225 230 235 240
 Phe Asp Lys Lys Leu Glu Ala Ser Arg Glu Glu Leu Thr Asp Ile Ala
 245 250 255
 Trp Ala Ser Thr Phe Thr Gln Ser Gln Thr Thr Pro Val Arg Asp Val
 260 265 270
 Asp Cys Val Ile Thr Thr Arg Glu Leu Leu Thr Leu Ala Thr Ala Arg
 275 280 285
 Gly Leu Ser Leu Pro Asn Leu Pro Leu Lys Pro Leu Pro Ala Ser Cys
 290 295 300
 Leu Thr Pro Phe Pro Asp Gln Ala Leu Glu Ser Phe Leu Phe Ser Lys
 305 310 315 320
 Ser Ser Ser Gly Gln Thr Val Glu Ser Gly Thr Ser Gly Gly Tyr Leu
 325 330 335
 His His Val Leu Gln Ile Phe Gln Ala Arg Asn Pro Gly Ser Lys Ile
 340 345 350
 Val Thr Gln Arg Gly Arg Asn Ala Asp Val Val Glu Tyr Val Leu Met
 355 360 365

Ser Ser Gly Asp Glu Pro Leu Phe Arg Ala Ala Arg Tyr Tyr Gly Phe
 370 375 380
 Arg Asn Ile Gln Asn Leu Val Arg Lys Leu Lys Pro Ala Arg Val Ser
 385 390 395 400
 Arg Leu Pro Gly Ala Lys Pro Gln Ala Val Ser Ser Ser Ala Asn Arg
 405 410 415
 Arg Gln Pro Met Ser Arg Asn Ala Ala Pro Ala Gly Thr Gly Ala Asp
 420 425 430
 Tyr Ala Tyr Val Glu Val Met Ala Cys Pro Gly Gly Cys Thr Asn Gly
 435 440 445
 Gly Gly Gln Ile Arg Ile Glu Asp Ala Arg Glu Ala Val Pro Asn Ala
 450 455 460
 Leu Lys Glu Thr Ser Thr Glu Thr Pro Val Ala Ala Pro Lys Pro Thr
 465 470 475 480
 Pro His Glu Gln Arg Ala Trp Leu Ala Arg Val Asp Glu Ala Tyr Tyr
 485 490 495
 Ser Ala Asp Ser Asp Ser Glu Gly Ser Val Thr Thr Glu Pro Val Ser
 500 505 510
 Val Leu Ser Arg Asp Asn Gln Ile His Glu Phe Leu Asn Tyr Trp Ser
 515 520 525
 Glu Lys Val Asp Ile Pro Leu Ser Arg Leu Ala Tyr Thr Ser Tyr Arg
 530 535 540
 Glu Val Glu Ser Asp Val Gly Lys Thr Lys Asn Ala Pro Asn Glu Thr
 545 550 555 560
 Ala Arg Val Val Glu Leu Ala Gly Lys Ile Gly Gly Gly Trp
 565 570

<210> 115

<211> 1510

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 115

taagagttgc	aggtatgagc	ctggtaaatac	aagtcagtc	cggatagcac	aacagaacct	60
cattttgtcc	tgaaagaatg	aaccaaaggg	ccaactcaga	ctctttgcaa	atgcaaggaa	120
gaggtaatga	gaatgttttg	ggagaagctt	aaatgtagct	ttgccggaac	ggagaattga	180
gtaaagccgg	tcatgaggcg	ccaagacccc	agcgaaaaag	cagccctagg	ccgcacgcaa	240
ccccgttcgg	cgagttgcta	ctggctgtta	agcgagactc	ttgtgggcga	agaccgcaac	300
acccgaaatt	cgcgatccag	tagcccagag	cgacttggtg	gcgtttcgga	cgactttgac	360
aatccccgact	cttcgacaac	aaattcccat	caccgccctc	ccggagtctg	tcgaccgtga	420
gtttgaaacc	tacgccctat	cgaatttctg	gactgtcact	gaagaatccg	tttttgcgt	480
tttttttagga	agccttcgcc	atggccgata	tcgatgtcaa	ggttgctcaa	tggaagcttg	540
ttgaggttgg	ccgtgtttgt	ctgatccgca	gcggtcctta	caccggcaag	cttgctgcca	600
ttgtcgagat	catcgaccac	aagcgtgtac	gtttttcaac	ggagaaattc	tgagcgcagg	660

acggaaagat	catgggtcggg	tgtgatattg	acaaagaggc	gcgatcatag	gtcctgggtg	720
acggtccttc	caccgaggag	aacaagatcg	ttccccgtca	cgctcttcct	ctcgctcacg	780
ccactctcac	ccccttcgtc	attcccaaac	tcccccgcg	tgccggcact	ggccccgtca	840
agaagctctg	ggagaagaac	gagatcgatg	gaaagtgggc	taagagcacc	attgctcaga	900
agactgagcg	cgctgagcgg	aggaagaacc	ttaccgactt	cgagcgcttc	aaggtcctca	960
gactcaagaa	gcaggtacgt	tcagtttgcg	aaactatggg	agaattgtga	tggcacattg	1020
gagggcattc	ttggcaactc	tgcactcgct	tttcgcgaga	gggaagagga	gcaattactt	1080
gtattatgat	ttgcgactgg	ttactgacat	ctggtgattt	aacaggctcg	ctacgaggtc	1140
cagaaggctc	acgccaaggt	cagggctgct	gctcctaagt	catagatggt	ttcatgaggc	1200
tcggtgcata	gtatgaaggg	gtaccttggg	acggttttac	atggctgagg	gttttattct	1260
atttcagcaa	aaattaagct	gtatccacta	caatgacagc	caaaaaatga	ttcaaacctt	1320
tgatatcctg	acacgggtca	tcctgctatg	tcatcagatt	cgcgaccccg	attagtactt	1380
ggctctggtt	tatagccgtc	tccttagaca	ttaattggga	attaaacatt	ttagactcaa	1440
gatcacggaa	tatgtaagaa	agtatcggtt	tgtacattac	tgagttggat	tggctcggtt	1500
tgactcgtat						1510

<210> 116

<211> 685

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
Genomic sequence containing the coding region

<400> 116

atggccgata	tcgatgtcaa	ggttgctcaa	tggaagcttg	ttgaggttgg	ccgtgttgtg	60
ctgatccgca	gcggtcctta	caccggcaag	cttgctgcca	ttgtcgagat	catcgaccac	120
aagcgtgtac	gtttttcaac	ggagaaattc	tgagcgcagg	acggaaagat	catgggtcggg	180
tgtgatattg	acaaagaggc	gcgatcatag	gtcctgggtg	acggtccttc	caccgaggag	240
aacaagatcg	ttccccgtca	cgctcttcct	ctcgctcacg	ccactctcac	ccccttcgtc	300
attcccaaac	tcccccgcg	tgccggcact	ggccccgtca	agaagctctg	ggagaagaac	360
gagatcgatg	gaaagtgggc	taagagcacc	attgctcaga	agactgagcg	cgctgagcgg	420
aggaagaacc	ttaccgactt	cgagcgcttc	aaggtcctca	gactcaagaa	gcaggtacgt	480
tcagtttgcg	aaactatggg	agaattgtga	tggcacattg	gagggcattc	ttggcaactc	540
tgcactcgct	tttcgcgaga	gggaagagga	gcaattactt	gtattatgat	ttgcgactgg	600
ttactgacat	ctggtgattt	aacaggctcg	ctacgaggtc	cagaaggctc	acgccaaggt	660
cagggctgct	gctcctaagt	catag				685

<210> 117

<211> 465

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
Coding region without introns

<400> 117

atggccgata	tcgatgtcaa	ggttgctcaa	tggaagcttg	ttgaggttgg	ccgtgttgtg	60
ctgatccgca	gcggtcctta	caccggcaag	cttgctgcca	ttgtcgagat	catcgaccac	120
aagcgtgtcc	tggttgacgg	tccttccacc	gaggagaaca	agatcgttcc	ccgtcacgct	180
cttctctctg	ctcacgccac	tctcaccccc	ttcgtcattc	ccaaactccc	ccgcgctgcc	240
ggcactggcc	ccgtcaagaa	gctctgggag	aagaacgaga	tcgatggaaa	gtgggctaag	300
agcaccattg	ctcagaagac	tgagcgcgct	gagcggagga	agaaccttac	cgacttcgag	360
cgcttcaagg	tcctcagact	caagaagcag	gctcgtacg	aggtccagaa	ggctcacgcc	420
aaggtcaggg	ctgctgctcc	taagtcatag	atgttttcat	gagggc		465

<210> 118

<211> 149
 <212> PRT
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619
 Protein sequence

<400> 118

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Met Ala Asp Ile Asp Val Lys Val Ala Gln Trp Lys Leu Val Glu Val
 1             5             10             15
Gly Arg Val Val Leu Ile Arg Ser Gly Pro Tyr Thr Gly Lys Leu Ala
          20             25             30
Ala Ile Val Glu Ile Ile Asp His Lys Arg Val Leu Val Asp Gly Pro
          35             40             45
Ser Thr Glu Glu Asn Lys Ile Val Pro Arg His Ala Leu Pro Leu Ala
          50             55             60
His Ala Thr Leu Thr Pro Phe Val Ile Pro Lys Leu Pro Arg Ala Ala
          65             70             75             80
Gly Thr Gly Pro Val Lys Lys Leu Trp Glu Lys Asn Glu Ile Asp Gly
          85             90             95
Lys Trp Ala Lys Ser Thr Ile Ala Gln Lys Thr Glu Arg Ala Glu Arg
          100            105            110
Arg Lys Asn Leu Thr Asp Phe Glu Arg Phe Lys Val Leu Arg Leu Lys
          115            120            125
Lys Gln Ala Arg Tyr Glu Val Gln Lys Ala His Ala Lys Val Arg Ala
          130            135            140

Ala Ala Pro Lys Ser
145

```

<210> 119
 <211> 1942
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
 Genomic sequence containing 3' and 5'-ends and the coding region

```

<400> 119
tacacccagc acacctaccc tagccacaga tttcttggac cacgggaacc cgaacaaaga      60
gtctctggcc gaactctggt ctaatttctt agagcaggag tcacaggcca gtgggaatcc      120
agaatcgccg aaaccatgaa gagtttcaaa aggtggctct gttctgagcc gtatagaaaa      180
ctagcatctt ctctaagata cggtaggtcc acatttatat atgcttgccg actggctttg      240
gtctcctctt cttttccatt ctagacttgc ttcgtagtaa taacactgat atcaccgcg      300
tgtttgcgac ttttgcacaa aaccagcttc cccaccgctt tctttctgcc accatagcgg      360
gggacctcgt tattgagcgg acaagtcgtc gttggctttt tctgcacggt tggcctatgc      420
ttcgtttatt cagctctggt acagctggga agttgactga tacactctcc tctctgattt      480
cttggtactc cagattgaca atgactaccg gggctggtac gatctctcat tccaacacct      540
atcatcgat  tcctcgccgt taactgacca atccaccagt gcaaagggtc cgtccagtgg      600
tggtatcggg tccctctggg actgggaagt cgaccttgct caagagactc ttcgctgaat      660

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accccgatac	tttcgattta	tccgtgtctc	gtacgtctaa	ccccttgcca	accctcattg	720
actatgcctg	cgaattgttt	cttttggttg	aattgcgctg	aacggtgttt	gttatattta	780
gataccactc	gagctccccg	tcccggggaa	gaaaatggac	gtgagtatta	cttcacaact	840
aaagaagatt	tcctggatct	tgtgagcaag	aatgccttta	tcgagcatgc	gcagtttggt	900
ggcaattact	acggtactac	tgtgcaggca	gtgaaggatg	ttgcgcagaa	gggcaagatc	960
tgcgttctcg	acattgagat	gaggtaataa	tagtcctgca	acgtgaactg	atatgaccgg	1020
agaagcagag	gaaatccatc	atcaaatgga	ttgtagtcca	acccaaacaa	cagctgacga	1080
ctgaattgca	atagggcggtg	aaacaagtca	agcgcaccga	tcttgatgct	cgattccttat	1140
tttttagcac	cccgtccctt	gaagaactag	agaaaagact	gcgtgggaga	gcaaccgaga	1200
ctgaggagag	cttgacggta	tggctgtcct	ccacattcct	tcacttcccc	aactcgccag	1260
actgtcccgc	tgggaattcta	actttgcgtc	agaaacgcct	tgcccaagct	aaaaatgaat	1320
tggaaatatg	ggcgcagcct	ggctctcatg	ataagattgt	cgtgaacgat	gacctggaga	1380
aggcttataa	ggaaactgcgg	gattggattg	tcgacgggtg	taactttgga	gcgcgtcaat	1440
gatttattgg	gcatgtctcg	gcgtgtttta	tttatcagcg	ctgctgtata	ctttagcgcc	1500
cgtagatact	gtcggttgcg	atactgaaaa	caatgcatca	tctgccttgg	taacttcggt	1560
ccacagaaac	ccataatcaa	ggaggtcctt	tcgtcgtcga	cgaacataag	agagattaat	1620
tacatgaaca	tcaagactat	gctaacaatt	cgaatgttgg	tctcttttct	gtctggagac	1680
gacaaatcta	ggaaagggtg	tagactcagt	cactctcttg	aacggagagg	agaaaattaa	1740
gcaaaactaa	aaaagagaac	aaagtctgat	gagcaatatg	agggctgaaa	aggatatctg	1800
taaagaggct	gctagaataa	aatggaagat	gccgattgag	aaggcaatgg	aggaagagaa	1860
gggggtcattt	atcgcagttt	ggcgtgggac	cagaaatgac	tgcagtatgt	ttatggacca	1920
tgccagcccg	agctattgga	ct				1942

<210> 120

<211> 943

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
Genomic sequence containing the coding region

<400> 120

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taactgacca	atccaccagt	gcaaagggtc	cgtccagtg	tggtatcggg	tccctctggg	120
actgggaagt	cgaccttgct	caagagactc	ttcgctgaat	accccgatac	tttcgattta	180
tccgtgtctc	gtacgtctaa	ccccttgcca	accctcattg	actatgcctg	cgaattgttt	240
cttttggtgg	aattgcgctg	aacggtgttt	gttatattta	gataccactc	gagctccccg	300
tcccggggaa	gaaaatggac	gtgagtatta	cttcacaact	aaagaagatt	tcctggatct	360
tgtgagcaag	aatgccttta	tcgagcatgc	gcagtttggt	ggcaattact	acggtactac	420
tgtgcaggca	gtgaaggatg	ttgcgcagaa	gggcaagatc	tgcgttctcg	acattgagat	480
ggaggtataa	atagtccctg	aacgtgaact	gatatgaccg	gagaagcaga	ggaaatccat	540
catcaaattg	attgtagtcc	aacccaaaca	acagctgacg	actgaattgc	aataggcggt	600
gaaacaagtc	aagcgcaccg	atcttgatgc	tcgattctta	tttttagcac	cccgtccct	660
tgaagaacta	gagaaaagac	tgcgtgggag	agcaaccgag	actgaggaga	gcttgacggt	720
atggctgtcc	tccacattcc	ttcacttccc	caactcgcca	gactgtcccc	ctggaattct	780
aactttgcgt	cagaaacgcc	ttgcccgaagc	taaaaatgaa	ttggaatatg	cggcgcagcc	840
tggctctcat	gataagattg	tcgtgaacga	tgacctggag	aaggcttata	aggaactgcg	900
ggattggatt	gtcgcaggtg	gtaacttttg	agcgcgtcaa	tga		943

<210> 121

<211> 603

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
Coding region without introns

```

<400> 121
atgactaccg gggctgtgca aaggttccgt ccagtgggtg tctcggtcc ctctgggact 60
gggaagtcga ccttgctcaa gagactcttc gctgaatacc ccgatacttt cgatttatcc 120
gtgtctcata ccaactcgagc tccccgtccc ggggaagaaa atggacgtga gtattacttc 180
acaactaaag aagatttcct ggatcttggt agcaagaatg cctttatcga gcatgcgag 240
tttgggtggca attactacgg tactactgtg caggcagtga aggatgttgc gcagaagggc 300
aagatctgcg ttctcgacat tgagatggag ggcgtgaaac aagtcaagcg caccgatctt 360
gatgctcgat tcttattttt agcaccctccg tcccttgaag aactagagaa aagactgcgt 420
gggagagcaa ccgagactga ggagagcttg acgaaacgcc ttgcccagc taaaaatgaa 480
ttggaatatg cggcgagcc tggtctcat gataagattg tcgtgaacga tgacctggag 540
aaggcttata aggaactgag ggattggatt gtcgacggtg gtaactttgg agcgcgtcaa 600
tga 603

```

<210> 122

<211> 200

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221
Protein sequence

<400> 122

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Met Thr Thr Gly Ala Val Gln Arg Phe Arg Pro Val Val Val Ser Gly
1          5          10          15

Pro Ser Gly Thr Gly Lys Ser Thr Leu Leu Lys Arg Leu Phe Ala Glu
      20          25          30

Tyr Pro Asp Thr Phe Asp Leu Ser Val Ser His Thr Thr Arg Ala Pro
      35          40          45

Arg Pro Gly Glu Glu Asn Gly Arg Glu Tyr Tyr Phe Thr Thr Lys Glu
      50          55          60

Asp Phe Leu Asp Leu Val Ser Lys Asn Ala Phe Ile Glu His Ala Gln
      65          70          75          80

Phe Gly Gly Asn Tyr Tyr Gly Thr Thr Val Gln Ala Val Lys Asp Val
      85          90          95

Ala Gln Lys Gly Lys Ile Cys Val Leu Asp Ile Glu Met Glu Gly Val
      100         105         110

Lys Gln Val Lys Arg Thr Asp Leu Asp Ala Arg Phe Leu Phe Leu Ala
      115         120         125

Pro Pro Ser Leu Glu Glu Leu Glu Lys Arg Leu Arg Gly Arg Ala Thr
      130         135         140

Glu Thr Glu Glu Ser Leu Thr Lys Arg Leu Ala Gln Ala Lys Asn Glu
      145         150         155         160

Leu Glu Tyr Ala Ala Gln Pro Gly Ser His Asp Lys Ile Val Val Asn
      165         170         175

Asp Asp Leu Glu Lys Ala Tyr Lys Glu Leu Arg Asp Trp Ile Val Asp
      180         185         190

```

Gly Gly Asn Phe Gly Ala Arg Gln
195 200

<210> 123
<211> 3108
<212> DNA
<213> *Aspergillus fumigatus*

<220>
<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 123
aaaccaggcg catatgttcc gctgccgccc tgcgcaggag agggctgata aggattgccca 60
tatccagacg acgggggctg ctgggatgct gggggaggag gcgagcgcat catgggaacg 120
gtagatacat gctgaggcac aggatgggtg agtggagggtg actgcgcagg cggtgggtgcg 180
aaagactggc ggtacatggt gatttttttt tcccttggtta caataagtga gaagctagtg 240
atgaacaaaa gacttgcgac tattctgtct cgtcttcttg tcttctacca accgaagagg 300
ggggatggtg gaaatcggac agtttgagta tgagtgatgt tgaagtgtgt ttatacgtgg 360
ctggactcgg tctgatcgcc ggagagctct caccttttcc gccacagggt cccaccata 420
gtggccacta cacacacttg tccgttctcc aaaaccacg ctgctcgac tgaataatat 480
acacaagaag tgcttacaac atgttagaag ccttcgaagt cttgacaaca tctgggggtg 540
tgctgtggtc gaagtcgtat gcgcgggtcg gagcgcatgt tgtcaacagc ctaatcaacg 600
atgtcttcat tgaggagaag gttcgagcgc agaatcaggc agcgagcagt gcagctccta 660
tctacaagaa ggaaaagtat actctgaaat ggaagcaagt aaaggatttc aatctgatat 720
ttgtggtatg ttcacgccgc tcgttgattc aatggcgcca ctgaccgatt ccataggctg 780
tatatcaatc tctgtacat cttggttggg tcgacaaact cttggataat gtttcgacca 840
tattcatcga cttatataag gatgagctaa ggagcacacg ggctaggatt attgagtacc 900
cattcgataa gtacttcgac cagcagggtgc gagagcttga ggacaatgct ggggctccta 960
catcagaatc tctcgtagta gagatcaacg agagaaagga cctcttctgt tcatcagata 1020
acggcgggcc acctccgcca cccgtgcctg gtctgtgtaa aggtatctga cgtcgataat 1080
ttttctctgc tagtgatcat attgctaact acctccgaag cgcaacgtcc agttgcgcag 1140
ggcgtggcga cctcggaacga gggttcgcca ccccaaacc cagatctttc tcgatcgtca 1200
acgcccattt caggtcatct attgaccgcg aaaggagggg ctgctggccg cgcctctcgt 1260
cgcgcacgca aagcggccaa cgcgagcgct accgctctt ctggagatga aagcattcgg 1320
aaggggaaaa cattgaaaaa tggaaaaaa atgcgcaagt gggatgctga tggctttgcg 1380
gatgaggacg acggcaaggt cctcgattac tccgccccg cagatggtga ggacgcaccg 1440
gctcctgtag tccaggtctgt tgcgcaggaa tccctggggac gccgaacagg caagggccaa 1500
tttgtgctga aagatctagg ggatgaagtc cattccattc ttgagaatgc tgatcatgaa 1560
aagacaaaagt cttcctcgtc cacgggcttt gttgggtctg gagtcaacgc acttgggtgga 1620
ttcttccgta atattgtcgg cggcaaggte cttactgagg ctgacttgga gaaacccttg 1680
aaagccatgg aagaccattt gctgaagaag aacgttgccg gcgaagcggc cgtccgtcta 1740
tgtcaaggcg tccagcgcca attagtgtgc aagaagacag gcaactttca aagtgttgat 1800
gcagactgc gtcgcgaat ggagtcctcg ttgcgcaaaa tattgacgcc aacgtcatct 1860
ctcgatctac tgcgtgagat cgatgctgtt agatctccga cgagcaaaag acaggctcct 1920
cgcccatatg tcatttccat cgtgggcgtg aacgggtgtg ggaagtcgac aaatctgggc 1980
aaaatttgtt acttccttct ccagaataac tatcgtgttc tgattgcagc ctgtgacacc 2040
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<210> 124

<211> 2059

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167
Genomic sequence containing the coding region

<400> 124

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<210> 125

<211> 1884

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167

Coding region without introns

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aaggctcctc attactccgc ccccgagat ggtgaggacg caccggctcc tgtagtcgag    780
gctgttgctc aggaatcctg gggacgccga acaggcaagg gccaatttgt gctgaaagat    840
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gtcggcggca agtcccttac tgaggctgac ttggagaaac ccttgaaagc catggaagac   1020
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gataccgttg gtgacatggt aggtacgctt gtcagcatgg tgcattgctac aggcattcct   1800
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<210> 126

<211> 641

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167
Protein sequence

<400> 126

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Ser Lys Ser Tyr Ala Pro Val Gly Ala His Val Val Asn Ser Leu Ile
          20          25          30

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Asn Asp Val Phe Ile Glu Glu Lys Val Arg Ala Gln Asn Gln Ala Ala
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Ser Ser Ala Ala Pro Ile Tyr Lys Lys Glu Lys Tyr Thr Leu Lys Trp
          50          55          60

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Lys Gln Val Lys Asp Phe Asn Leu Ile Phe Val Ala Val Tyr Gln Ser

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65	70	75	80
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Ile Phe Ile Asp Leu Tyr Lys Asp Glu Leu Arg Ser Thr Arg Ala Arg	100	105	110
Ile Ile Glu Tyr Pro Phe Asp Lys Tyr Phe Asp Gln Gln Val Arg Glu	115	120	125
Leu Glu Asp Asn Ala Gly Ala Pro Thr Ser Glu Ser Leu Val Val Glu	130	135	140
Ile Asn Glu Arg Lys Asp Pro Leu Val Ser Ser Asp Asn Gly Gly Pro	145	150	155
Pro Pro Pro Pro Val Pro Val Ala Gln Gly Val Ala Thr Ser Asp Glu	165	170	175
Gly Ser Pro Pro Gln Thr Pro Asp Leu Ser Arg Ser Ser Thr Pro Ile	180	185	190
Ser Gly His Leu Leu Thr Ala Lys Gly Gly Pro Ala Gly Arg Ala Ser	195	200	205
Arg Arg Ala Arg Lys Ala Ala Asn Ala Ser Ala Thr Ala Ser Ser Gly	210	215	220
Asp Glu Ser Ile Arg Lys Gly Lys Thr Leu Lys Ser Gly Lys Lys Met	225	230	235
Arg Lys Trp Asp Ala Asp Gly Phe Ala Asp Glu Asp Asp Gly Lys Val	245	250	255
Leu Asp Tyr Ser Ala Pro Ala Asp Gly Glu Asp Ala Pro Ala Pro Val	260	265	270
Val Glu Ala Val Ala Gln Glu Ser Trp Gly Arg Arg Thr Gly Lys Gly	275	280	285
Gln Phe Val Leu Lys Asp Leu Gly Asp Glu Val His Ser Ile Leu Glu	290	295	300
Asn Ala Asp His Glu Lys Thr Lys Ser Ser Ser Ser Thr Gly Phe Val	305	310	315
Gly Ser Gly Val Asn Ala Leu Gly Gly Phe Phe Arg Asn Ile Val Gly	325	330	335
Gly Lys Val Leu Thr Glu Ala Asp Leu Glu Lys Pro Leu Lys Ala Met	340	345	350
Glu Asp His Leu Leu Lys Lys Asn Val Ala Arg Glu Ala Ala Val Arg	355	360	365
Leu Cys Gln Gly Val Gln Arg Glu Leu Val Gly Lys Lys Thr Gly Asn	370	375	380
Phe Gln Ser Val Asp Ala Ala Leu Arg Ser Ala Met Glu Ser Ser Leu	385	390	395
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Arg Lys Ile Leu Thr Pro Thr Ser Ser Leu Asp Leu Leu Arg Glu Ile
 405 410 415
 Asp Ala Val Arg Ser Pro Thr Ser Lys Gly Gln Ala Pro Arg Pro Tyr
 420 425 430
 Val Ile Ser Ile Val Gly Val Asn Gly Val Gly Lys Ser Thr Asn Leu
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 Gly Lys Ile Cys Tyr Phe Leu Leu Gln Asn Asn Tyr Arg Val Leu Ile
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 Ala Ala Cys Asp Thr Phe Arg Ser Gly Ala Val Glu Gln Leu Arg Val
 465 470 475 480
 His Ala Arg Asn Leu Lys Glu Leu Ser Thr Arg Glu Asn Ala Gly Glu
 485 490 495
 Val Glu Leu Tyr Glu Lys Gly Tyr Gly Lys Asp Ala Ala Asn Val Ala
 500 505 510
 Lys Asp Ala Val Glu Tyr Gly Ala Ala Asn His Phe Asp Val Val Leu
 515 520 525
 Ile Asp Thr Ala Gly Arg Arg His Asn Asp Gln Arg Leu Met Ser Ser
 530 535 540
 Leu Glu Lys Phe Ala Lys Phe Ala Lys Pro Asp Lys Ile Phe Met Val
 545 550 555 560
 Gly Glu Ala Leu Val Gly Thr Asp Ser Val Met Gln Ala Arg Asn Phe
 565 570 575
 Asn Gln Ala Phe Gly Thr Gly Arg Asn Leu Asp Gly Phe Ile Ile Ser
 580 585 590
 Lys Cys Asp Thr Val Gly Asp Met Val Gly Thr Leu Val Ser Met Val
 595 600 605
 His Ala Thr Gly Ile Pro Ile Val Phe Leu Gly Val Gly Gln His Tyr
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 Lys

<210> 127

<211> 2564

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 127

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gatgattccg	attattgtga	aactgggtta	aatcgcgcca	gaggggcagg	tatcgtgacg	240
gagagggggt	atatcgtcga	atggagggtt	tgagtgcaga	cggccgacga	ttgcgcagtt	300
caaagcggcg	aagaggtctt	ggcactctcg	gtccaaacac	gttgcccgtt	ctctccaact	360
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cagaaaagga	attatactcg	aaattatggg	ctgacctaga	aggtgctcta	acctactgaa	660
cttctacggt	aataatgtaa	tattaattgg	tagctcgagg	atataacctc	gacttcgaat	720
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<210> 128

<211> 1564

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
 Genomic sequence containing the coding region

<400> 128

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tattaattgg	tagctcgagg	atataacctc	gacttcgaat	ccccaagaa	tgacaagctc	240
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aagggttagc	gttaccctta	gacatgtcca	tatgctctgc	tttgtacatc	tcaattgacc	360
tcttgccag	gctatggacc	ctcccttacc	cccaagaata	tcattgattt	catgaacaag	420

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<210> 129

<211> 1383

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
Coding region without introns

<400> 129

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aagttgaggt ccgataccaa ggctttcttt gatggcgagg gcgttgtagc atttcccaga 540
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<210> 130

<211> 460

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
Protein sequence

<400> 130

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Arg Ala Leu Ser Ser Ser Gly Ser Arg Leu Leu Val Val Leu Glu Asp
20 25 30

Ala Thr Glu Lys Glu Leu Tyr Ser Lys Leu Trp Ala Asp Leu Glu Gly
35 40 45

Tyr Asn Leu Asp Phe Glu Ser Pro Lys Asn Asp Lys Leu Ser Leu Phe
50 55 60

Glu Leu Gly Asp Arg Val Tyr Asp His Met Leu Leu Leu Pro Pro Lys
65 70 75 80

Ser Lys Gly Tyr Gly Pro Ser Leu Thr Pro Lys Asn Ile Ile Asp Phe
85 90 95

Met Asn Lys Asp Gly Asn Val Leu Leu Ala Leu Ser Gly Lys Ser Thr
100 105 110

Thr Ala Ser Ala Ile Ser Ser Leu Leu Leu Glu Leu Asp Leu His Leu
115 120 125

Pro Val Asp Arg Ser Ser Val Thr Val Asp His Phe Asn Tyr Asp Thr
130 135 140

Leu Ser Ala Ser Asp Lys His Asp Val Leu Leu Leu His Arg Pro Gly
145 150 155 160

Lys Leu Arg Ser Asp Thr Lys Ala Phe Phe Asp Gly Glu Gly Val Val
165 170 175

Ala Phe Pro Arg Ala Val Pro His Thr Leu Gly Asp Ala Asn Pro Leu
180 185 190

Ile Ala Pro Ile Leu Arg Ala Pro Ala Thr Ala Tyr Ser Tyr Asn Pro
195 200 205

Lys Glu Asp Ala Ser Ser Val Glu Asp Val Ala Ala Thr Gly Ser Gln
210 215 220

Leu Ala Leu Val Ser Ala Met Gln Ala Arg Asn Ser Ala Arg Phe Thr
225 230 235 240

Leu Leu Gly Ser Val Glu Ser Leu Gln Asp Gln Trp Phe Ser Ala Thr
245 250 255

Val Lys Ala Pro Gly Asp Gly Lys Gln Met Lys Thr Val Asn Gln Glu
260 265 270

Phe Ala Lys Gln Leu Thr Ala Trp Thr Phe Lys Glu Thr Gly Val Leu
275 280 285

Lys Val Gly Lys Ile Glu His His Leu Ala Glu Asp Gly Glu Ile Thr
290 295 300

Pro Glu Lys Leu Asn Pro Lys Ile Tyr Arg Ile Lys Asn Glu Thr Val
305 310 315 320

Phe Ser Ile Glu Leu Ser Glu Tyr Asn Tyr Asp Arg Tyr Ala Pro Phe
325 330 335

Glu Val Pro Thr Gly Asp Ala Val Gln Leu Glu Phe Thr Met Leu Ser
340 345 350

Pro Phe His Arg Leu Asn Leu Glu Pro Val Arg Arg Thr Asp Asn Ser
355 360 365

Thr Val Tyr Ser Thr Arg Phe Thr Thr Pro Asp Gln His Gly Ile Phe
370 375 380

Ser Phe Arg Val Asn Tyr Lys Arg Pro Phe Leu Thr Asn Ile Glu Glu
385 390 395 400

Lys Leu Glu Val Thr Val Arg His Phe Ala His Asn Glu Tyr Pro Arg
405 410 415

Ser Trp Lys Ile Ser Gly Gly Trp Val Trp Ile Ala Gly Leu Trp Ser
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Val Ile Ala Gly Phe Leu Val Phe Val Val Ala Trp Leu Tyr Ser Ala
435 440 445

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<210> 131

<211> 3376

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 131

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<210> 132

<211> 2376

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737
 Genomic sequence containing the coding region

<400> 132

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<210> 133

<211> 2148

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737

Coding region without introns

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aagcgctcgt	atgcatccgt	cgaggagaac	cttgcccgtc	tcgaggagat	gaagaagggt	1020

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<210> 134

<211> 715

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737
Protein sequence

<400> 134

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Ser Pro Val Ile Ser Ile Thr Tyr Glu Asp Thr Ala Val Leu Arg Glu
35        40        45

Gly Asp Lys Ala Val Val Gln Tyr Thr Gly Ala Ser Gly Asn Pro Ile
50        55        60

Phe Gly Leu Ile Asn Ala Val Gln Glu Leu Arg Lys Asp Phe Pro Phe
65        70        75        80

Leu Asn Ser Lys Asp Glu Lys Leu Glu Asn Glu Trp Leu Ser Gln Leu
85        90        95

Glu Ala Phe Ala Pro Leu Asp Phe Lys Ala Leu Asp Pro Glu Leu Gln
100       105       110

Arg Leu Asp Thr His Leu Leu Leu Arg Ser Phe Val Val Gly Tyr Ala
115       120       125

Leu Ser Thr Ala Asp Ile Ala Leu Trp Gly Ala Ile Arg Gly Asn Arg
130       135       140

Val Ala Val Ala Ala Ile Lys Lys Gly Ser Leu Val Asn Val Thr Arg

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	180	185			190	
Glu Gly Ala Ser Tyr Asp Ile Ala Leu Leu Asn Thr Glu Lys Gly Val						
	195	200			205	
Val Thr Arg Phe Pro Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His						
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Ala Lys Ala Ala Leu Leu Asn Asp Tyr Phe Ala His Glu Lys Tyr Asn						
	225	230			235	240
Gly Thr Leu Leu Val Arg Phe Asp Asp Thr Asn Pro Ser Asn Glu Lys						
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Leu Glu Phe Gln Asp Ala Ile Ile Glu Asp Leu Ala Leu Met Gly Ile						
	260	265			270	
Lys Pro Asp Lys Met Ser Tyr Thr Ser Asp Tyr Phe Asp Glu Leu Tyr						
	275	280			285	
Gln Tyr Ala Leu Gln Ile Ile Lys Asp Gly Asn Ala Tyr Ala Asp Asp						
	290	295			300	
Thr Glu Lys Glu Val Met Ala Glu Gln Arg Met Asn Gly Lys Pro Ser						
	305	310			315	320
Lys Arg Arg Asp Ala Ser Val Glu Glu Asn Leu Ala Arg Phe Glu Glu						
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Met Lys Lys Gly Thr Pro Glu Gly Leu Arg Trp Cys Ile Arg Ala Lys						
	340	345			350	
Met Ser Val Asp Asn Pro Asn Lys Ala Met Arg Asp Pro Val Ile Tyr						
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Arg Cys Asn Pro Ala Pro His His Arg Thr Gly Thr Lys Trp Lys Ile						
	370	375			380	
Tyr Pro Thr Tyr Asp Phe Ala Cys Pro Ile Val Asp Ser Ile Glu Gly						
	385	390			395	400
Val Thr His Ala Leu Arg Thr Ile Glu Tyr Arg Asp Arg Asn Pro Gln						
	405	410			415	
Tyr Gln Trp Phe Leu Asp Thr Leu Lys Leu Arg His Val Gln Ile Trp						
	420	425			430	
Asp Phe Ala Arg Met Asn Phe Ile Arg Thr Leu Leu Ser Lys Arg Lys						
	435	440			445	
Leu Thr Lys Leu Val Asn Gln Gly Val Val Trp Gly Trp Asp Asp Pro						
	450	455			460	
Arg Phe Pro Thr Ile Arg Gly Ile Arg Arg Arg Gly Met Thr Ile Pro						
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Ala Leu Arg Glu Phe Ile Leu Lys Gln Gly Pro Ser Lys Asn Ile Thr
485 490 495

Asn Leu Asp Trp Thr Leu Ile Trp Ala Thr Asn Lys Lys Tyr Ile Asp
500 505 510

Pro Val Ala Pro Arg His Thr Ala Ile Leu Lys Lys Asp Met Val Lys
515 520 525

Ala Ile Val Lys Gly Gly Pro Ala Thr Pro Tyr Thr Glu Glu Lys Pro
530 535 540

Lys His Gly Lys Asn Pro Ala Val Gly Met Lys Lys Val Val Phe Gly
545 550 555 560

Asn Thr Val Ile Phe Asp Gln Lys Asp Ala Lys Ser Phe Lys Gln Asp
565 570 575

Glu Glu Ile Thr Leu Met Ser Trp Gly Asn Ala Ile Val Arg Lys Ile
580 585 590

Glu Thr Asp Pro Thr Ser Gly Ile Val Lys Glu Leu Glu Leu Glu Leu
595 600 605

His Leu Glu Gly Asp Phe Lys Lys Thr Glu Lys Lys Val Thr Trp Leu
610 615 620

Ser Thr Glu Gly Gln Asp Leu Ile Pro Val Glu Leu Val Asp Phe Asp
625 630 635 640

Tyr Leu Leu Asn Lys Asp Thr Leu Gln Glu Asp Asp Val Leu Glu Asp
645 650 655

Val Leu Asn Lys Asn Thr Glu Phe Arg Glu Asp Ala Val Ala Asp Cys
660 665 670

Asn Val Ala Glu Leu Lys Glu Gly Asp Ile Ile Gln Phe Glu Arg Lys
675 680 685

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690 695 700

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<210> 135

<211> 3639

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 135

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<210> 136

<211> 2639

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446
Genomic sequence containing the coding region

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<210> 137

<211> 2430

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446

Coding region without introns

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<210> 138

<211> 809

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446
Protein sequence

<400> 138

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<210> 139

<211> 2684

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
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<400> 139

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<210> 140

<211> 1707

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
Genomic sequence containing the coding region

<400> 140

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1707

<210> 141

<211> 1707

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
Coding region without introns

<400> 141

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<210> 142

<211> 568

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
Protein sequence

<400> 142

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Glu	Leu	Gln	Tyr	Asp	Val	Leu	Gln	Leu	Ser	Asp	Arg	Val	Asn	Glu	Leu
		20						25					30		

Asn	Ser	Leu	His	Gly	Thr	Arg	Asp	Leu	Leu	Glu	Lys	Ile	Lys	Gln	Met	35	40	45
Pro	Val	Thr	Leu	Pro	Glu	Asp	Thr	Leu	Glu	Thr	Tyr	Glu	Phe	Asn	His	50	55	60
Leu	Leu	Arg	Asn	Val	Lys	Glu	Ala	Thr	Leu	Val	Leu	Arg	Asn	Met	Val	65	70	75
Leu	Leu	Lys	Glu	Asn	Ala	Tyr	Tyr	Val	Ser	Arg	Tyr	Ala	Lys	Gly	Leu	85	90	95
Leu	Arg	Asp	Phe	Leu	Val	Ile	Met	Ile	Asn	Leu	Pro	Asn	Gln	Pro	Arg	100	105	110
Leu	Asn	Glu	Ile	Lys	Asn	Asp	Ala	Leu	Asp	Ile	Ala	Glu	Glu	Val	Thr	115	120	125
Lys	Phe	Met	Lys	Thr	Asp	Pro	Glu	Asp	Pro	Leu	Trp	Ile	Ser	Leu	Leu	130	135	140
Asn	Cys	Leu	Gly	Ser	Ser	Asp	Arg	Ala	His	Val	Val	Arg	Ala	Leu	Trp	145	150	155
Ala	Leu	Thr	His	Phe	Ser	Thr	Glu	Leu	Asp	Glu	Pro	Glu	Ala	Asn	Arg	165	170	175
Ala	Met	Glu	Arg	Ile	Pro	Lys	Glu	Thr	Leu	Gln	Gln	Leu	Tyr	Phe	His	180	185	190
Thr	Leu	Leu	Asp	Leu	Asp	Lys	Asp	Ile	Leu	Ser	Gly	Ala	Leu	Asp	Phe	195	200	205
Trp	Tyr	Gln	Tyr	Thr	Leu	Ser	Ser	Glu	Asn	Ile	Glu	Thr	Leu	Ile	Glu	210	215	220
Val	Phe	Asn	Leu	Pro	Thr	Val	Phe	Val	Pro	Arg	Met	Val	Ala	Leu	Leu	225	230	235
Thr	His	Glu	Gly	Arg	Pro	Asn	Lys	Lys	Glu	Thr	Val	Leu	Gln	Glu	Glu	245	250	255
Lys	Val	Ala	Pro	Pro	Pro	Ser	Asp	Ile	Pro	Arg	Val	Pro	Pro	Glu	Leu	260	265	270
Met	Lys	Glu	Leu	Met	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Ser	Ser	Arg	Trp	275	280	285
Leu	Arg	Cys	Cys	Phe	Val	Glu	Asp	Leu	Glu	Cys	Glu	Ile	Thr	Gln	Ile	290	295	300
Ala	Leu	Trp	Gln	Ala	Tyr	Gln	Ser	Arg	Phe	Ala	Asp	Pro	Arg	Leu	Pro	305	310	315
Gly	Gly	Gly	Val	Leu	Pro	Ala	Ala	Glu	Phe	Ile	Lys	Asn	Val	Ser	Thr	325	330	335
Thr	Phe	Thr	Asn	Ala	Gln	Ala	Gln	Val	Ile	Asn	Gly	Pro	Gly	Ala	Ala	340	345	350

Thr Lys Phe Ile Ile Lys Gly Ile Arg Pro Leu Glu Thr Ala Tyr Thr
 355 360 365
 Phe Glu Gly Phe Pro Tyr Ile Tyr Cys Lys Trp Ala Asp Asn Ser Lys
 370 375 380
 Pro Ser Lys Thr Cys Gln Arg Ala Phe Lys Ser Pro Ala Glu Leu Arg
 385 390 395 400
 His His Val Phe Thr Glu His Met Asn Leu Lys Pro Thr Glu Thr Pro
 405 410 415
 Gly His Tyr Asn Leu Glu Lys Ala Glu Ser Pro Val His Thr Cys Leu
 420 425 430
 Trp Asp Asn Cys Thr Lys Phe Arg Ser Ser Gly Pro Ser Ala Asn Thr
 435 440 445
 Ala Met Val Ala Gly His Val Ser Ala His Leu Pro Glu Glu Arg Ala
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 Pro Asp Ala Glu Pro Pro Thr Ser Lys Arg Ala Val Leu Gln Glu Arg
 465 470 475 480
 Ile Val Arg Lys Trp Tyr Tyr Leu Asp Thr Pro Val Asn Glu Arg Gly
 485 490 495
 Glu Pro Phe Gly Val Ala Tyr Lys Ala Ala Leu Val Leu Arg Asn Leu
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 Ala Arg Asn Leu Pro Thr Gly Ile Ala Pro Gln Tyr Asn Gly Leu Ser
 515 520 525
 Trp Lys Lys Ala Val Phe Leu Ser His Arg Pro Lys Ile Ile Glu Ala
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<210> 143

<211> 2542

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 143

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acgagggtgc	tcggcatata	gtcacaattc	ctttttcaag	aggctttttc	ctcctctccc	240
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caccactgcg	ttgctcctca	tctcaataat	cggctcttgca	ccagcatacg	tcacacaatt	480

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<210> 144

<211> 1542

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
Genomic sequence containing the coding region

<400> 144

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<210> 145

<211> 1482

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
Coding region without introns

<400> 145

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ggtccagaga aactcttgga ggtgtggttc gcgccttcgc ctccaggaatt aggtccagcg 180
cagcccgcgc gtctgaaggc tgttcggag gagatctgga aggacatgtt ggatctcgtc 240
aattgccagg tcctctcgat tgtttcgtca gaggatgtgg acgcctacct gctctccgag 300
tctagcatgt tcgtttggcc tcacaaactc atcttgaaga cttgtggtac caccactctt 360
ctgtctggtc tcccacgcat tctcgagatt gccgctttgt tcggtggctt ccccaagtct 420
accgcccctt ctcgcggaat ctccgtcgcc gctgcgcctt accgcgtctt ctacagccgc 480
aagaacttcc tgttccccga ccgccagcgg ggcctcacc gcagctggag agatgaagtg 540
cggactatgg ataagctctt cctcaacggc agcgcctaca tgattggcaa gatgaatggc 600
gagcactggt acttgtacct gactgaacct cataccatgc tcaccccgcc aacgagcccg 660
ggagccaaga ccgagtttac ggaaacggag accaaggtec tcagtgtacc ccaggcgcgt 720
gctctcgaca ctgattcgga ggatgagact ttggaagtct tgatgaccga cttggatgag 780
gagaacgcca agcagttcta cctcgagaat gccactgccg ttgcggagaa ccgttatcgc 840
aactcaaatt cggagaagag tggccatggt gatgttttca gcaacacttc ctccgatatc 900
agcgattttg actccgacgg aagccagggt ctgcctccag agttgactac cgagggtcac 960
gcgctcggaa ccgtggtctc tgaagcctgt ggactttcct ctgtgtatcc taaggagaag 1020
tatcccgatt cgcgcacga tgcctacctg tttacaccat gcggcttctc cgccaacggc 1080
gtgattccgc ctctgagggg aaaagctgga acccactact tcacagtaca cgtcactcca 1140
gagccgcact gttcatatgc gtcctttgag accaacgtac cgcactcgca gaacggccag 1200
actaccgctg gaatcatcaa gcaagtgggc gacatcttca agcctggtcg cttcagcgtg 1260
actctcttcg aggccaaagg agcgtgagc caggtcgaag acgagtggaa ggaagccaag 1320
tacctggccg ctcgctcggac cgccaaaatg gaacatgtgg agggatatcg ccgagtggac 1380
cggattgtcc acgacctcga cggctatgag cttgtcttcc gctattatga acgcctggac 1440
tggaaagggg gggccctcgc gctgggagag gagagatctt ga 1482

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<210> 146

<211> 493

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101
Protein sequence

<400> 146

Met Val Tyr Ile Gly Ile Pro Lys Asn Tyr Thr Ala Ser Pro Ser Ser
 1 5 10 15
 Phe Ala Gly Thr Pro Ser Leu Thr Ile Asn Tyr Glu Ala Thr Gln Asp
 20 25 30
 Leu Asp Ser Thr Asn Ala Phe Glu Gly Pro Glu Lys Leu Leu Glu Val
 35 40 45
 Trp Phe Ala Pro Ser Ala Gln Glu Leu Gly Pro Ala Gln Pro Ala Gly
 50 55 60
 Leu Lys Ala Val Pro Glu Glu Ile Trp Lys Asp Met Leu Asp Leu Val
 65 70 75 80
 Asn Cys Gln Val Leu Ser Ile Val Ser Ser Glu Asp Val Asp Ala Tyr
 85 90 95
 Leu Leu Ser Glu Ser Ser Met Phe Val Trp Pro His Lys Leu Ile Leu
 100 105 110
 Lys Thr Cys Gly Thr Thr Thr Leu Leu Ser Gly Leu Pro Arg Ile Leu
 115 120 125
 Glu Ile Ala Ala Leu Phe Gly Gly Phe Pro Lys Ser Thr Ala Pro Ser
 130 135 140
 Arg Gly Ile Ser Val Ala Ala Ala Pro Tyr Arg Val Phe Tyr Ser Arg
 145 150 155 160
 Lys Asn Phe Leu Phe Pro Asp Arg Gln Arg Gly Pro His Arg Ser Trp
 165 170 175
 Arg Asp Glu Val Arg Thr Met Asp Lys Leu Phe Leu Asn Gly Ser Ala
 180 185 190
 Tyr Met Ile Gly Lys Met Asn Gly Glu His Trp Tyr Leu Tyr Leu Thr
 195 200 205
 Glu Pro His Thr Met Leu Thr Pro Pro Thr Ser Pro Gly Ala Lys Thr
 210 215 220
 Glu Phe Thr Glu Thr Glu Thr Lys Val Leu Ser Val Pro Gln Gly Ala
 225 230 235 240
 Ala Leu Gln Thr Asp Ser Glu Asp Glu Thr Leu Glu Val Leu Met Thr
 245 250 255
 Asp Leu Asp Glu Glu Asn Ala Lys Gln Phe Tyr Leu Glu Asn Ala Thr
 260 265 270
 Ala Val Ala Glu Asn Arg Tyr Arg Asn Ser Asn Ser Glu Lys Ser Gly
 275 280 285
 His Val Asp Val Phe Ser Asn Thr Ser Ser Asp Ile Ser Asp Phe Asp
 290 295 300
 Ser Asp Gly Ser Gln Val Leu Pro Pro Glu Leu Thr Thr Glu Gly His
 305 310 315 320

Ala Leu Gly Thr Val Val Ser Glu Ala Cys Gly Leu Ser Ser Val Tyr
 325 330 335

Pro Lys Glu Lys Tyr Pro Asp Ser Arg Ile Asp Ala Tyr Leu Phe Thr
 340 345 350

Pro Cys Gly Phe Ser Ala Asn Gly Val Ile Pro Pro Pro Glu Gly Lys
 355 360 365

Ala Gly Thr His Tyr Phe Thr Val His Val Thr Pro Glu Pro His Cys
 370 375 380

Ser Tyr Ala Ser Phe Glu Thr Asn Val Pro His Ser Gln Asn Gly Gln
 385 390 395 400

Thr Thr Ala Gly Ile Ile Lys Gln Val Val Asp Ile Phe Lys Pro Gly
 405 410 415

Arg Phe Ser Val Thr Leu Phe Glu Ala Lys Pro Ala Leu Ser Gln Val
 420 425 430

Glu Asp Glu Trp Lys Glu Ala Lys Tyr Leu Ala Ala Arg Arg Thr Ala
 435 440 445

Lys Met Glu His Val Glu Gly Tyr Arg Arg Val Asp Arg Ile Val His
 450 455 460

Asp Leu Asp Gly Tyr Glu Leu Val Phe Arg Tyr Tyr Glu Arg Leu Asp
 465 470 475 480

Trp Lys Gly Gly Ala Pro Arg Leu Gly Glu Glu Arg Ser
 485 490

<210> 147

<211> 1637

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 147

aaagatagag	aagacgttgc	gcggaacctt	ttgaggaccc	tcagctctat	ttgagtgtct	60
gtcacgaggt	ccatatctgg	cgatacggag	ggctggctgt	acaattaggt	tactcttatt	120
tcctactgat	ctagtgatat	aaagtttggg	tgcattatgt	aaattaaatc	tcgggggcaa	180
atgaacattt	cgaatatcgt	tataaaactc	acagaaagtg	ctgtcaatgg	cacaaattta	240
gcaatcaata	ctcatctgag	tatgttggtg	ataagtccga	aaacaaccta	aatattttacc	300
tcattaggaa	aggtgcactc	cgtagttacc	tcgactcgcg	gttagtctgg	tgactaagtt	360
cttggcgttg	tgatgagggc	aagtcctatc	atgtgatcat	agttagggtt	tccacacacc	420
aggctctcca	atatagcaag	aaaatagaag	gattagggtc	cgtctccgaa	catccatccc	480
gccagcacac	aaccgcctaaa	atgggtcgcg	ttagaaccga	ggtaagttac	agatgaagca	540
tcataagtta	tcttcaaaaa	agccccaaga	gagtatcatt	tctgacgaaa	tgggtttttc	600
ttcaatagac	agtcaagagg	tccgccaagg	tcacatcgga	gcgctactac	cccaagttga	660
cgctcgactt	tgagaccaac	aagcgtcttt	gcgatgagat	cgctatcatt	gcctccaagc	720
gccttcgcaa	caaggtgggc	aatccatcac	tgagccgtac	aacagtcgga	atttgacttg	780
ctgacgaaaa	ctagattgct	ggttacacca	cccaccttat	gaagcgtatc	cagcgtggcc	840
ctgtccgcgg	tatctctttc	aagctgcagg	aggaggagcg	tgagcgcaag	gatcagtagc	900
ttcctgaggt	ttccgctctg	gatgtttccc	agaccgagtc	cggccagctc	gatgtcgatg	960
ccgacaccaa	ggaccttctc	aagtccatgg	gcgtaagttc	tggttctcaac	gcggttggtc	1020

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gtgggttttaa agcagtcctgt taacttatat tgcccactac agttcgacaa tctcaaggtc 1080
aacgttgttca acgtctccca acatcagggt caggagcgcc cccgccgctt ccggtagatg 1140
cgcgaccccc tcgagcctcg aaaaaaaagt taccgattgt cttcggtcga tctatggcgt 1200
gctcaatcac acttgctctg gctgacttcg cagctatgat gtagcctaga gacacaggaa 1260
tgaacataat tctctctgag aaaggtgtcg ctgattctcc tgggtggagat gacgcttgat 1320
tgccaaaatt tctccttttg cttactgtcc gtttcagctc gggcgctgcg tagaagggtc 1380
tctctgcatg atgcgcagga tgtcatcaga gagtcgaaac ctttgggtgcg aactgcacca 1440
tcaactgcac cgcattggat cagatccata ttaatcagtc tatctacaga agtaaattgg 1500
gtatcgtcat aagcacaaag acgccgtaga accacaaatc gaaccacccc atcgaattct 1560
gtcgtgacca ggctcacgcc aaaccgcgtg agattgaagc atatcatgat cagatttcc 1620
ttggcacgta gccttca 1637

```

<210> 148

<211> 637

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827
Genomic sequence containing the coding region

<400> 148

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atggggtcgcg ttagaaccaa ggtaagttac agatgaagca tcatgagtta tcttcaaaaa 60
agcccaaaaa gagtatcatt tctgacgaaa tgggtttttc ttcaatagac agtcaagagg 120
tccgccaaagg tcatcatcga gcgctactac cccaagttga cgctcgactt tgagaccaac 180
aagcgtcttt gcgatgagat cgctatcatt gcctccaagc gccttcgcaa caagggtgggc 240
aatccatcac tgagccgtac aacagtcgga atttgacttg ctgacgaaaa ctagattgct 300
ggttacacca cccaccttat gaagcgtatc cagcgtggcc ctgtccgcgg tatctctttc 360
aagctgcagg aggaggagcg tgagcgcaag gatcagtagc ttctgaggt ttccgctctg 420
gatgtttccc agaccgagtc cggccagctc gatgtcgatg ccgacaccaa ggaccttctc 480
aagtccatgg gcgtaagttc tgttctcaac gcggttggtc gtgggtttta agcagtcctgt 540
taacttatat tgcccactac agttcgacaa tctcaaggtc aacgttgta acgtctccca 600
acatcagggt caggagcgcc cccgccgctt ccggtag 637

```

<210> 149

<211> 420

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827
Coding region without introns

<400> 149

```

atggggtcgcg ttagaaccaa gacagtcaag aggtccgcca aggtcatcat cgagcgctac 60
taccceaagt tgacgctcga ctttgagacc aacaagcgtc ttgcgatga gatcgctatc 120
attgcctcca agcgccttcg caacaagatt gctgggtaca ccacccacct tatgaagcgt 180
atccagcgtg gccctgtccg cggatatctt ttcaagctgc aggaggagga gcgtgagcgc 240
aaggatcagt acgttcctga ggtttccgct ctggatgttt ccagaccga gtccggccag 300
ctcgatgtcg atgccgacac caaggacctt ctcaagtcca tgggcttcga caatctcaag 360
gtcaacgttg tcaacgtctc ccaacatcag gttcaggagc gcccccgccg cttccggtag 420

```

<210> 150

<211> 139

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827

Protein sequence

<400> 150

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Met Gly Arg Val Arg Thr Lys Thr Val Lys Arg Ser Ala Lys Val Ile
 1              5              10              15
Ile Glu Arg Tyr Tyr Pro Lys Leu Thr Leu Asp Phe Glu Thr Asn Lys
          20              25              30
Arg Leu Cys Asp Glu Ile Ala Ile Ile Ala Ser Lys Arg Leu Arg Asn
          35              40              45
Lys Ile Ala Gly Tyr Thr Thr His Leu Met Lys Arg Ile Gln Arg Gly
          50              55              60
Pro Val Arg Gly Ile Ser Phe Lys Leu Gln Glu Glu Arg Glu Arg
65              70              75              80
Lys Asp Gln Tyr Val Pro Glu Val Ser Ala Leu Asp Val Ser Gln Thr
          85              90              95
Glu Ser Gly Gln Leu Asp Val Asp Ala Asp Thr Lys Asp Leu Leu Lys
          100              105              110
Ser Met Gly Phe Asp Asn Leu Lys Val Asn Val Val Asn Val Ser Gln
          115              120              125
His Gln Val Gln Glu Arg Pro Arg Arg Phe Arg
          130              135

```

<210> 151

<211> 2037

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 151

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aaggtagtag gtgcagatat tgttgataga catttcaaaa tgtattagtt acatgattac      60
ttacttagat gtaatctttc gataataact tctagtcttg ttgagttcag aaggccagtg      120
tgtgctgaaa atgacagcga cctatgcggt gcccggtgtag cgaagagcac tggctggaaa      180
taagaagttt attagaggag cctcatgatg cataatcatt gtaagcgcac gatgcacaat      240
aatatatccg aatttctcca gatgacacta agataataac gaaaatatca catgacgttg      300
tgggcaggta tgtattatgt aatctgatcg gtagggccga tgtctcgctt agcggacttt      360
tctgtgggat tgcaatttca acttattatt ccgccgacca gcaacaaagc ggttactcga      420
ctcgactccc tccaccagag cccgtggtgt gatatacctg tctgtctttg atcctcgcaa      480
gatagacttg agtcgcagtt atggcggttg gaaagtatgc caattcactt ctattattgt      540
tctgaacgct tttagcatgt gtctggatac ggtggtttac aggtactgat ccgggaacag      600
gaacaagcgc ttgtcgaagg gcaagaaggg tgtaagaagg aggaccgttg atcctttctc      660
caggaaggac gaataactctg ttaaggtagt tcgacgtgga ctgtgtaagt cgaccgcagc      720
taatctatat caggcgctt ccactttcca gatcagagag tatgttgcac gcatatgatg      780
tcgaattgca ggataaaggc gattcacaat ggtagtgag attatgctga ctgaattata      840
gtgtcgggaa gactctggtc aaccgcacca gtggtctcaa gaacgccaat gactccctga      900
agggtcgaat tttcagagtc tcgctggctg acctgcagaa tgatgaagac catgctttcc      960
gcaaggttaa gcttcgtgtg gacgaggttc agggcaagaa ctgtttgacc aacttccacg      1020
gtcttgattt cacaaccgac aaattgcgat ccctcgtcg caagtggcag tcgctgatcg      1080
aagccaatgt cactgtgaag acgaccgatg attatctcct tcggcttttt gctatcgctt      1140

```

tcaccaagag	acgcccgaac	cagattaaga	agaccacata	tgctcgttct	tctcaaatacc	1200
gtgccatccg	caagaagatg	attgaaatca	tgagagggga	ggcagccagc	tgctctctcg	1260
ctcagctcac	tcacaagctc	attcctgagg	tcattgggtcg	tgagatcgag	aaggctaccc	1320
agggaaatcta	tcctttgcag	aatgtgtgtg	accctgttat	tcttactcgg	gatgaagact	1380
aactgcaatc	taggtccata	ttcgcaaggt	caagcttctt	aaggctccca	agttcgacct	1440
gggtgcactg	ctgaatctgc	acggtgaatc	tacaaccgat	gataagggcc	acaaggtcga	1500
gagagagttc	aaggagcagg	ttctcgaaag	cgtttaagtg	gactgaatta	ccagtatgct	1560
ggttattcgg	gacattgatt	tgtacctacc	tgtatgcttg	gattcttttt	ttatgagtta	1620
aaatgggaaa	agaacttttg	tcgcggcatc	atgtctttat	tgactgggtg	tgctcgtaac	1680
ttctatgtcc	tttgagaatg	gagcttgcaa	agaaaacttt	gcccttattc	aaatatttaa	1740
ttggacaatt	ccgatcaaa	tttagcagta	gaataacctgc	tataccagtg	atgtgctgat	1800
gcaacgggca	cctgcagttt	actttcagtt	gattcaaatt	ctatattaac	agagcccttt	1860
taccacacca	ctgacctggg	attagtatag	tgtctcgccc	taggagacta	aagaattgct	1920
agaagtatgg	ttatacataa	tggtgaatag	ttagtatgat	ttattaatat	tattttcagt	1980
gcactgatat	atatcataat	gctactaaat	atagctaccc	taagatttat	atagaga	2037

<210> 152

<211> 1037

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18

Genomic sequence containing the coding region

<400> 152

atggcggttg	gaaagtatgc	caattcactt	ctattattgt	tctgaacgct	tttagcatgt	60
gtctggatac	ggtggtttac	aggtactgat	ccgggaacag	gaacaagcgc	ttgtcgaagg	120
gcaagaagg	tgtaagaag	aggaccgttg	atcctttctc	caggaaggac	gaatactctg	180
ttaaggtatg	tcgacgtgga	ctgtgtaagt	cgaccgcagc	taatctatat	caggcgctt	240
ccactttcca	gatcagagag	tatgttgca	gcataatgatg	tcgaattgca	ggataaaggc	300
gattcacaat	ggtagtggag	attatgctga	ctgaattata	gtgtcgggaa	gactctggtc	360
aaccgcacca	gtggtctcaa	gaacgccaat	gactccctga	agggtcgaat	tttcgaggtc	420
tcgctggctg	acctgcagaa	tgatgaagac	catgctttcc	gcaagggttaa	gcttcgtgtg	480
gacgaggttc	agggcaagaa	ctgtttgacc	aacttccacg	gtcttgattt	cacaaccgac	540
aaattgcgat	ccctcgtgcg	caagtggcag	tcgctgatcg	aagccaatgt	caactgtgaag	600
acgaccgatg	attatctcct	tcggcttttt	gctatcgctt	tcaccaagag	acgcccgaac	660
cagattaaga	agaccacata	tgctcgttct	tctcaaatacc	gtgccatccg	caagaagatg	720
attgaaatca	tgagagggga	ggcagccagc	tgctctctcg	ctcagctcac	tcacaagctc	780
attcctgagg	tcattgggtcg	tgagatcgag	aaggctaccc	agggaaatcta	tcctttgcag	840
aatgtgtgtg	accctgttat	tcttactcgg	gatgaagact	aactgcaatc	taggtccata	900
ttcgcaaggt	caagcttctt	aaggctccca	agttcgacct	gggtgcactg	ctgaatctgc	960
acggtgaatc	tacaaccgat	gataagggcc	acaaggtcga	gagagagttc	aaggagcagg	1020
ttctcgaaag	cgttttaa					1037

<210> 153

<211> 771

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18

Coding region without introns

<400> 153

atggcggttg	gaaagaacaa	gcgcttgctg	aagggcaaga	aggggtgttaa	gaagaggacc	60
gttgatcctt	tctccaggaa	ggacgaatac	tctgttaagg	cgccttccac	tttccagatc	120
agagatgtcg	ggaagactct	ggtcaaccgc	accagtggtc	tcaagaacgc	caatgactcc	180
ctgaagggtc	gaattttcga	ggtctcgctg	gctgacctgc	agaatgatga	agacctgct	240

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ttccgcaagg ttaagcttcg tgtggacgag gttcagggca agaactgttt gaccaacttc 300
cacggtcttg atttcacaac cgacaaattg cgatccctcg tgcgcaagtg gcagtcgctg 360
atcgaagcca atgtcactgt gaagacgacc gatgattatc tccttcggct ttttgctatc 420
gccttcacca agagacgccc gaaccagatt aagaagacca catatgctcg ttcttctcaa 480
atccgtgcca tccgcaagaa gatgattgaa atcatgcaga gggaggcagc cagctgctct 540
ctcgctcagc tcactcacia gctcattcct gaggtcattg gtcgtgagat cgagaaggct 600
acccagggaa tctatccttt gcagaatgtc catattcgca aggtcaagct tcttaaggct 660
cccaagttcg acctgggtgc actgctgaat ctgcacggtg aatctacaac cgatgataag 720
ggccacaagg tcgagagaga gttcaaggag caggttctcg aaagcgttta a 771

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<210> 154

<211> 256

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18
Protein sequence

<400> 154

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Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Val
1          5          10          15
Lys Lys Arg Thr Val Asp Pro Phe Ser Arg Lys Asp Glu Tyr Ser Val
20          25          30
Lys Ala Pro Ser Thr Phe Gln Ile Arg Asp Val Gly Lys Thr Leu Val
35          40          45
Asn Arg Thr Ser Gly Leu Lys Asn Ala Asn Asp Ser Leu Lys Gly Arg
50          55          60
Ile Phe Glu Val Ser Leu Ala Asp Leu Gln Asn Asp Glu Asp His Ala
65          70          75          80
Phe Arg Lys Val Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Cys
85          90          95
Leu Thr Asn Phe His Gly Leu Asp Phe Thr Thr Asp Lys Leu Arg Ser
100         105         110
Leu Val Arg Lys Trp Gln Ser Leu Ile Glu Ala Asn Val Thr Val Lys
115         120         125
Thr Thr Asp Asp Tyr Leu Leu Arg Leu Phe Ala Ile Ala Phe Thr Lys
130         135         140
Arg Arg Pro Asn Gln Ile Lys Lys Thr Thr Tyr Ala Arg Ser Ser Gln
145         150         155         160
Ile Arg Ala Ile Arg Lys Lys Met Ile Glu Ile Met Gln Arg Glu Ala
165         170         175
Ala Ser Cys Ser Leu Ala Gln Leu Thr His Lys Leu Ile Pro Glu Val
180         185         190
Ile Gly Arg Glu Ile Glu Lys Ala Thr Gln Gly Ile Tyr Pro Leu Gln
195         200         205

```

Asn Val His Ile Arg Lys Val Lys Leu Leu Lys Ala Pro Lys Phe Asp
 210 215 220

Leu Gly Ala Leu Leu Asn Leu His Gly Glu Ser Thr Thr Asp Asp Lys
 225 230 235 240

Gly His Lys Val Glu Arg Glu Phe Lys Glu Gln Val Leu Glu Ser Val
 245 250 255

<210> 155

<211> 1819

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 155

aattcatcag	cataacgaac	ccccaacgac	ttcgaaaaaa	aagcccgatt	cgaaagaatt	60
gcgcattcaa	cataccatgg	tgggcggctt	cgtgtcgtgt	cgtacgggta	ttgtcgacaa	120
tgaggattga	agatgggcca	ggtcaatttg	ggatgttcgt	tgtgggacta	gggttttttt	180
ctgtgttggt	gcggtcacgc	tgcggctggg	ctaagcgggc	acgtgactgt	ggctgactgc	240
ctggtgacgc	ccccccccgg	aggaaccccc	aaccggcagc	cagataggct	cgggaggatc	300
atcgtcgaat	gatggcattg	ttcttgggtc	cagtggatgg	gttattaatg	actgcctgga	360
cggctggatg	actccgtcgc	tgatttagca	ttgtgatcca	cgatttatgt	ttcatttctg	420
gggcgcgggt	ttactaccat	cacttttgtc	actaccatca	cttttatact	gagtttctga	480
ccccgacccc	gaaccagact	atggcaactt	cgactgggac	cggatgggct	cagctccggc	540
agcaagcccc	ttcgcttgag	actcagggtac	ggaactcgaa	actacgctat	aatgaggcct	600
tactcgtgat	ttggatggtg	acaataatgt	tcctagaccg	agagtctgtt	tcacacctat	660
gcgcagtatg	catcgatgac	gaagctgcct	ccgaaaccct	cagaagaaga	acaacggatt	720
gaatcgcaac	tgaaggatct	tcttgaaaag	gtgtgcaact	tgaggccctc	tagtccagcc	780
caacagacga	tcatgctgac	acgatccgat	catagcgtga	agccctcatc	tcccagctct	840
cccgtctcct	tgactccgaa	gccactctta	ccgcactctgc	cctgaaacag	agcaatcttg	900
cccgcgaatc	cgaagtccct	caggatcatc	gccgcgaatt	gcagcgcctg	aacgcgcgaa	960
tgcgccagtc	ccgcgaccga	gccaatcttc	tgtctaacgt	ccgctccgac	attgatgcct	1020
accgcaattc	aaaccccgcc	gcggctgagg	cagactacat	gctcgaggag	cgggggtcgta	1080
tagatgaaag	ccataacatg	atagatggtg	tcctaagcca	ggcgtatgca	atcaacgaga	1140
gttttgggct	acaacgtgaa	accctggcca	gcatcaatcg	ccgtatcgtc	ggtgctgcca	1200
ataaggtacc	aggaatgaat	gcattgattg	gtaagattgg	gacgaagagg	agacgtgacg	1260
caatcatctt	gggggctttc	atcggctttt	gtttcttgat	ggtgttcttc	ttccgatgag	1320
atgctgggtc	tccgtatacc	gccgatcttc	ctgtgttata	attccttgct	caacgttatc	1380
tacatcggag	accgcacggc	gttcgggtgt	tttcatgtac	tccttttctg	catgcaagca	1440
ctaatacaca	tggtcatggc	gtttcagggt	gtctatttca	catttatgta	catacagggt	1500
cagactgctg	tagccctagg	gtcaccgca	tgatcactct	tggtttcgga	cttgcggtt	1560
caccttggtt	tcttcccgcc	cattcctcag	ccggtagctt	cgactcgaga	ctgattcttc	1620
tctcctggat	taatttgcca	accccggtgt	tcaatccgtc	tagctcgctt	tcctctgccg	1680
gcccgtacc	cgcccatcgg	atgacgacgt	tctcgtccag	cagatagaca	taaccaactt	1740
tactgttcat	cattccgatt	gcttctttca	acccatccgt	aagacctttg	cgcacaagga	1800
aataccgttc	gtgctgctc					1819

<210> 156

<211> 819

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
 Genomic sequence containing the coding region

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<400> 156
atggcaactt cgactgggac cggatgggct cagctccggc agcaagcccg ttcgcttgag    60
actcaggtac ggaactcgaa actacgctat aatgaggctt tactcgtgat ttggatgttg    120
acaataatgt tcctagaccg agagtctgtt tcacacctat gcgcagtatg catcgatgac    180
gaagctgcct ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct    240
tcttgaaaag gtgtgcactt tgaggccctc tagtccagcc caacagacga tcatgctgac    300
acgatccgat catagcgtga agccctcatc tcccagctct cccgtctcct tgactccgaa    360
gccactctta ccgcatctgc cctgaaacag agcaatcttg cccgcaatcg cgaagtcctc    420
caggatcatc gccgcgaatt gcagcgccctg aacgccgcaa tcgccgagtc ccgcgaccga    480
gccaatcttc tgtctaacgt ccgctccgac attgatgcct accgcaattc aaaccccgcc    540
gcggctgagg cagactacat gctcgaggag cggggtcgta tagatgaaag ccataacatg    600
atagatggtg tcctaagcca ggcgatgca atcaacgaga gttttgggct acaacgtgaa    660
accctggcca gcatcaatcg ccgtatcgtc ggtgctgcca ataaggtacc aggaatgaat    720
gcattgattg gtaagattgg gacgaagagg agacgtgacg caatcatctt gggggctttc    780
atcggtttt gtttcttgat ggtgttcttc ttccgatga    819

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<210> 157

<211> 684

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
Coding region without introns

```

<400> 157
atggcaactt cgactgggac cggatgggct cagctccggc agcaagcccg ttcgcttgag    60
actcagaccg agagtctgtt tcacacctat gcgcagtatg catcgatgac gaagctgcct    120
ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct tcttgaaaag    180
cgtgaagccc tcatctccca gctctcccg tctcttgact ccgaagccac tcttaccgca    240
tctgccttga aacagagcaa tcttgcccg aatcgcgaa tcttccagga tcatcgccgc    300
gaattgcagc gcctgaacgc cgcaatcgcc gagtcccgcg accgagccaa tcttctgtct    360
aacgtccgct ccgacattga tgctaccgc aattcaaacc ccgccgcgcc tgaggcagac    420
tacatgctcg aggagcgggg tcgtatagat gaaagccata acatgataga tgggtgccta    480
agccaggcgt atgcaatcaa cgagagtttt gggctacaac gtgaaaccct ggccagcatc    540
aatcgccgta tcgtcggtgc tgccaataag gtaccaggaa tgaatgcatt gattggtaag    600
attgggacga agaggagacg tgacgcaatc atcttggggg ctttcatcgg cttttgtttc    660
ttgatggtgt tcttcttccg atga    684

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<210> 158

<211> 227

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250
Protein sequence

<400> 158

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Met Ala Thr Ser Thr Gly Thr Gly Trp Ala Gln Leu Arg Gln Gln Ala
1          5          10          15

```

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Arg Ser Leu Glu Thr Gln Thr Glu Ser Leu Phe His Thr Tyr Ala Gln
20          25          30

```

```

Tyr Ala Ser Met Thr Lys Leu Pro Pro Lys Pro Ser Glu Glu Glu Gln
35          40          45

```

Arg Ile Glu Ser Gln Leu Lys Asp Leu Leu Glu Lys Arg Glu Ala Leu
 50 55 60
 Ile Ser Gln Leu Ser Arg Leu Leu Asp Ser Glu Ala Thr Leu Thr Ala
 65 70 75 80
 Ser Ala Leu Lys Gln Ser Asn Leu Ala Arg Asn Arg Glu Val Leu Gln
 85 90 95
 Asp His Arg Arg Glu Leu Gln Arg Leu Asn Ala Ala Ile Ala Glu Ser
 100 105 110
 Arg Asp Arg Ala Asn Leu Leu Ser Asn Val Arg Ser Asp Ile Asp Ala
 115 120 125
 Tyr Arg Asn Ser Asn Pro Ala Ala Ala Glu Ala Asp Tyr Met Leu Glu
 130 135 140
 Glu Arg Gly Arg Ile Asp Glu Ser His Asn Met Ile Asp Gly Val Leu
 145 150 155 160
 Ser Gln Ala Tyr Ala Ile Asn Glu Ser Phe Gly Leu Gln Arg Glu Thr
 165 170 175
 Leu Ala Ser Ile Asn Arg Arg Ile Val Gly Ala Ala Asn Lys Val Pro
 180 185 190
 Gly Met Asn Ala Leu Ile Gly Lys Ile Gly Thr Lys Arg Arg Arg Asp
 195 200 205
 Ala Ile Ile Leu Gly Ala Phe Ile Gly Phe Cys Phe Leu Met Val Phe
 210 215 220
 Phe Phe Arg
 225

<210> 159

<211> 2601

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 159

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tctgcctcc	ttttcgctt	ctttttttcc	cctttttatc	ttttcathtt	atcatctttg	120
ttactgtttt	cccaaacgaa	tccattatta	tttttttccc	ttggagggtc	cctactgtgg	180
tcttgtgtct	gcactcttgc	caagcccatt	ggtccttgct	ctgagcctat	cacttgcgat	240
tcgcccgc	ataagtccgc	ctctctcaac	ctttccatct	cacgcgcacc	tccactcaac	300
atccaccatt	cggatattcc	gcccatccaa	agcgaacacc	cctccttctg	ctccaccatc	360
gattgcagtc	tgcccaaaac	ggacttcaga	actcccttct	acgctathtt	ccgccattca	420
ctgttgaagt	gcagccctcc	atactctcga	tagcaactgc	ccaaccccc	tcttactgcc	480
aacccccacaa	gttgcccg	atgtcacaaa	atcgacctgg	ggtgttctcg	aatctgcgca	540
tgggtggtaa	ggaacatcca	aatgctgagt	ccaattgttc	agaaaacatt	accaggagc	600
ctgtggaact	aactgctttg	ctttccgacc	atacagaagt	cgtccgcgag	aagggtccagg	660
atggactgac	aggggaaact	aaggagattt	cgtactcaca	atgtaaaatc	gtcggcaatg	720
gatcggttgg	tgtcgtcttt	cagacgaaaa	tgatgccaag	cggcgaggat	gctgccatta	780
agaggtcct	tcaagacaag	cgcttcaaag	tatgtgtaca	ttataagggc	aattgccttc	840

gctgcccac	ccaaagatac	tgtcgctgac	gagataccag	aatcgagaac	tgcagattat	900
gcggattgtt	cgccatccta	acatcgtaga	attgaaagcc	ttctattact	cgaacggcga	960
gagggtatgc	gactctcctt	tgtctcccca	ttcgttctag	tttgccgttt	gctgactacc	1020
ctaccattgt	ctttcacaga	aggatgaagt	gtacctaaac	ctcgttctcg	aatacgtacc	1080
agaaaccgtg	tatcgggcgt	cgcggtactt	taataaactc	aaaacgacta	tgccaatggt	1140
ggaaagtcaag	ctgtatatct	atcaattggt	ccgttccctg	gcatacatcc	attcacaagg	1200
catctgccac	cgtgacatca	agccccagaa	tctcttactt	gatccatcca	ccggcatcct	1260
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aaagatcggg	aagtcttgac	tgattcctcc	ttcaagtttg	gtactgtcat	gctgacgac	1440
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tccctggaga	gtcgggaatt	gaccaactgg	tggaaatcat	caaggttctt	ggaaccctta	1560
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caaattcatt	cttccagatg	gcttattcgc	tgatcactct	ttttagaac	tttctattgc	1980
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gcactttttc	cgaacgtatg	aggatacaag	gcaaattcccc	atatttaaaa	gaaaaaggag	2340
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gtcatagtct	ggagttttcg	aggtgtctga	gacagctctt	gggaaaggaa	aaaaagtgat	2520
accctttagt	gtgcgagtct	gccttcgggg	atttaagttt	gcatagcttc	attctcgttt	2580
gaaggaggac	atgaccattc	c				2601

<210> 160

<211> 1601

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439

Genomic sequence containing the coding region

<400> 160

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ctttccgacc	atacagaagt	cgctccgcgag	aagggtccagg	atggactgac	aggggaaact	180
aaggagattt	cgtactcaca	atgtaaaatc	gtcggcaatg	gatcgttttg	tgtcgtcttt	240
cagacgaaaa	tgatgccaag	cggcgaggat	gctgccatta	agagggtcct	tcaagacaag	300
cgcttcaaa	tatgtgtaca	ttataagggc	aattgccctc	gctgcccac	ccaaagatac	360
tgtcgctgac	gagataccag	aatcgagaac	tgcagattat	gcggattgtt	cgccatccta	420
acatcgtaga	attgaaagcc	ttctattact	cgaacggcga	gagggtatgc	gactctcctt	480
tgtctcccca	ttcgttctag	tttgccgttt	gctgactacc	ctaccattgt	ctttcacaga	540
aggatgaagt	gtacctaaac	ctcgttctcg	aatacgtacc	agaaaccgtg	tatcgggcgt	600
cgcggtactt	taataaactc	aaaacgacta	tgccaatggt	ggaagtcaag	ctgtatatct	660
atcaattggt	ccgttccctg	gcatacatcc	attcacaagg	catctgccac	cgtgacatca	720
agccccagaa	tctcttactt	gatccatcca	ccggcatcct	caaactctgc	gactttgggt	780
cggccaaagt	tctggtagag	aatgagccca	acgtttccta	tatctgttcc	cgctactatc	840
gtgcgcggga	attgatcttt	ggcgccacta	attacacaac	aaagatcggg	aagtcttgac	900
tgattcctcc	ttcaagtttg	gtactgtcat	gctgacgac	gtcaagacgt	gtggtccacg	960
ggttgtgtga	tggctgaact	catgcttggg	cagccattgt	tccctggaga	gtcgggaatt	1020
gaccaactgg	tggaaatcat	caaggttctt	ggaaccctta	ctcgggagca	gatccgcacc	1080
atgaacccaa	actatatgga	gcacaaattc	cctcaaataca	agccacaccc	attcaacaag	1140

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gtgaccacgc tcttaaagaa cttcttgcca atatgcactg acttgatgac cccagggttt 1200
ccggagagct cctcacgagg ccattgatct gatctcagct ttgctagaat acacgccgac 1260
acaacgtctc tccgctatcg aggcgatgtg ccacccgttc ttcgacgaac tcagagatcc 1320
caatacgcga ctgcccgaact ctcggcaccc tgggtggcgt gctagagacc tccccaatct 1380
ctttgatttc tccagacatg gtttgttgtc acttgaggcc caaattcatt cttccagatg 1440
gcttattcgc tgatcactct tttgtagaac tttctattgc acctgcattg aacagccggc 1500
tggttcccc tcatgcacgc gccgctctcg aggcccgagg gctagacatt gacaacttca 1560
ctcctctcac gaaggaggag atgatggcac gtctcgactg a 1601

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<210> 161

<211> 1185

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439
Coding region without introns

<400> 161

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gtcggcaatg gatcgtttgg tgcgtcttt cagacgaaaa tgatgccaa ggcgaggat 180
gctgccatta agagggctct tcaagacaag cgcttcaaaa atcgagaact gcagattatg 240
cggattgttc gccatcctaa catcgtagaa ttgaaagcct tctattactc gaacggcgag 300
aggaaggatg aagtgtacct aaacctcgtt ctcgaatacg taccagaaac cgtgtatcgg 360
gcgtcgcggt actttaataa actcaaaacg actatgccaa tgttggaagt caagctgtat 420
atctatcaat tgttccgttc cctggcatac atccattcac aaggcatctg ccaccgtgac 480
atcaagcccc agaattctctt acttgatcca tccaccggca tctcaaaact ctgcgacttt 540
ggttcggcca agattctggt agagaatgag cccaacgttt cctatatctg tccccgctac 600
tatcgtgcgc cggaattgat ctttggcgcc actaattaca caacaaagat cgacgtgtgg 660
tccacgggtt gtgtgatggc tgaactcatg cttggtcagc cattgttccc tggagagtcg 720
ggaattgacc aactgggtgga aatcatcaag gttcttgga cccctactcg ggagcagatc 780
cgcaccatga acccaaaacta tatggagcac aaattccctc aaatcaagcc acaccattc 840
aacaagggtt tccggagagc tcctcacgag gccattgatc tgatctcagc tttgctagaa 900
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cggctgggtt cccctcatgc acgcgccgct ctcgaggccc gggggctaga cattgacaac 1140
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<210> 162

<211> 394

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439
Protein sequence

<400> 162

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1           5           10           15
Val Val Arg Glu Lys Val Gln Asp Gly Leu Thr Gly Glu Thr Lys Glu
20           25           30
Ile Ser Tyr Ser Gln Cys Lys Ile Val Gly Asn Gly Ser Phe Gly Val
35           40           45

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Val Phe Gln Thr Lys Met Met Pro Ser Gly Glu Asp Ala Ala Ile Lys
 50 55 60
 Arg Val Leu Gln Asp Lys Arg Phe Lys Asn Arg Glu Leu Gln Ile Met
 65 70 75 80
 Arg Ile Val Arg His Pro Asn Ile Val Glu Leu Lys Ala Phe Tyr Tyr
 85 90 95
 Ser Asn Gly Glu Arg Lys Asp Glu Val Tyr Leu Asn Leu Val Leu Glu
 100 105 110
 Tyr Val Pro Glu Thr Val Tyr Arg Ala Ser Arg Tyr Phe Asn Lys Leu
 115 120 125
 Lys Thr Thr Met Pro Met Leu Glu Val Lys Leu Tyr Ile Tyr Gln Leu
 130 135 140
 Phe Arg Ser Leu Ala Tyr Ile His Ser Gln Gly Ile Cys His Arg Asp
 145 150 155 160
 Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Ser Thr Gly Ile Leu Lys
 165 170 175
 Leu Cys Asp Phe Gly Ser Ala Lys Ile Leu Val Glu Asn Glu Pro Asn
 180 185 190
 Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala Pro Glu Leu Ile Phe
 195 200 205
 Gly Ala Thr Asn Tyr Thr Thr Lys Ile Asp Val Trp Ser Thr Gly Cys
 210 215 220
 Val Met Ala Glu Leu Met Leu Gly Gln Pro Leu Phe Pro Gly Glu Ser
 225 230 235 240
 Gly Ile Asp Gln Leu Val Glu Ile Ile Lys Val Leu Gly Thr Pro Thr
 245 250 255
 Arg Glu Gln Ile Arg Thr Met Asn Pro Asn Tyr Met Glu His Lys Phe
 260 265 270
 Pro Gln Ile Lys Pro His Pro Phe Asn Lys Val Phe Arg Arg Ala Pro
 275 280 285
 His Glu Ala Ile Asp Leu Ile Ser Ala Leu Leu Glu Tyr Thr Pro Thr
 290 295 300
 Gln Arg Leu Ser Ala Ile Glu Ala Met Cys His Pro Phe Phe Asp Glu
 305 310 315 320
 Leu Arg Asp Pro Asn Thr Arg Leu Pro Asp Ser Arg His Pro Gly Gly
 325 330 335
 Ala Ala Arg Asp Leu Pro Asn Leu Phe Asp Phe Ser Arg His Glu Leu
 340 345 350
 Ser Ile Ala Pro Ala Leu Asn Ser Arg Leu Val Pro Pro His Ala Arg
 355 360 365

Ala Ala Leu Glu Ala Arg Gly Leu Asp Ile Asp Asn Phe Thr Pro Leu
 370 375 380

Thr Lys Glu Glu Met Met Ala Arg Leu Asp
 385 390

<210> 163

<211> 2539

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 163

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gcgctgtggc	atggcgatcc	gatcagggag	atgatgacat	cgtggacagg	ttgtgggaga	180
gcggacgaga	taggacggag	aacgggttga	agagggtcaa	taacgacctt	ttgaagcgta	240
tccatggcga	gagttctacag	ggcaaaagac	ggctcagggc	cttggttgaa	gaggagtgtg	300
ccaacggagc	acgggtggttc	caaaagatca	gcaacaacca	tcgggacgga	atggtgcatt	360
cattcctgcg	gttgtggtct	ctgtgcctcg	ccggggaatt	tctgccctgt	caatcgcgac	420
tcttccgaga	ctcactatct	catgatctag	atctcgtcct	atcgtgattt	caatatccct	480
ccgtccatgt	tccttccgcc	atgatttatt	tccggtcctc	gttgctgagg	tctggattgg	540
ctcgagatcc	tgctcgctg	tggtcacaat	gcttctcacg	actctcacca	tcacgacgac	600
ctgtcgcagt	tcgcagcttc	ttctcctcat	ctcggctgcg	ggctggcatt	gccgatcatg	660
aatcaactcc	ctcgactgtc	caaaagacct	atttttctgc	caatcggacc	gcagatggct	720
tacttgcatc	cttatccgcc	gtcaatagct	cccctcgaag	tattgccgac	aatgcgttat	780
cacagggtgc	agccagttcg	gagtcgatta	cttcacagtc	tacttcacaa	gagttacctc	840
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tggtgacgac	tacctccgct	tatgggatgt	acccgatctc	ctctcttctc	acacttgacc	1080
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acgatgccct	catgtcacgg	acacggaacc	ggccggttagt	gcgggggcta	ctctcacgcc	1260
gtgctgcggt	attgtttgcg	attgcgactg	ctgctgcagg	tctcggtttg	ttatacattg	1320
gaacgaaccc	tacgactact	gcgctctccg	ccagtaatat	ctgtctctat	gcctttgtgt	1380
atacgccgct	gaagcgtata	tcagtgatca	acacctgggt	aggcgccgtg	gtaggaggca	1440
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<210> 164

<211> 1539

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
Genomic sequence containing the coding region

<400> 164

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<210> 165

<211> 1539

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
Coding region without introns

<400> 165

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accctctcga	cctcaacctt	gacctttctc	tacctgacca	caggaacctt	cttgtcttca	660
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gtcgggtggc tggtcacgaa gaaaggtctc tgggatggtg tctggaacaa tgttttcggt     1440
cagcctgtgg aagacgagga tgactatctc tgggaggatg aggatgaagt ggcagaggcg     1500
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<210> 166

<211> 512

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190
Protein sequence

<400> 166

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Arg Pro Val Ala Val Arg Ser Phe Phe Ser Ser Ser Arg Leu Arg Ala
35              40              45

Gly Ile Ala Asp His Glu Ser Thr Pro Ser Thr Val Gln Lys Thr Tyr
50              55              60

Phe Ser Ala Asn Arg Thr Ala Asp Gly Leu Leu Ala Ser Leu Ser Ala
65              70              75              80

Val Asn Ser Ser Pro Arg Ser Ile Ala Asp Asn Ala Leu Ser Gln Gly
85              90              95

Ala Ala Ser Ser Glu Ser Ile Thr Ser Gln Ser Thr Ser Gln Glu Leu
100             105             110

Pro His Arg Arg Arg Lys Arg Leu Lys Glu Glu Ala Ala Lys Asn Asn
115             120             125

Ala Ala Glu Thr Glu Leu Pro Pro Asp Ala Ser Ser Gln Leu Ser Thr
130             135             140

Leu Ser Ser Ala Leu Pro Ala Thr Ser Leu Arg Arg Lys Leu Ala Ala
145             150             155             160

Phe Leu Ala Leu Thr Lys Pro Arg Leu Ser Phe Leu Ile Val Leu Thr
165             170             175

Thr Thr Ser Ala Tyr Gly Met Tyr Pro Ile Ser Ser Leu Leu Thr Leu

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210					215					220					
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225					230					235					
Thr	Arg	Asn	Arg	Pro	Leu	Val	Arg	Gly	Leu	Leu	Ser	Arg	Arg	Ala	Ala
245					250					255					
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260					265					270					
Ile	Gly	Thr	Asn	Pro	Thr	Thr	Thr	Ala	Leu	Ser	Ala	Ser	Asn	Ile	Cys
275					280					285					
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325					330					335					
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405					410					415					
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420					425					430					
Tyr	Lys	Phe	Trp	Arg	His	Gln	Gly	Ala	Asn	Gly	Ser	Ala	Arg	Arg	Leu
435					440					445					
Phe	Trp	Ala	Ser	Ile	Trp	Gln	Leu	Pro	Ile	Leu	Leu	Val	Gly	Gly	Leu
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Val	Thr	Lys	Lys	Gly	Leu	Trp	Asp	Gly	Val	Trp	Asn	Asn	Val	Phe	Gly
465					470					475					
Gln	Pro	Val	Glu	Asp	Glu	Asp	Asp	Tyr	Leu	Trp	Glu	Asp	Glu	Asp	Glu
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<210> 167
 <211> 2679
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
 Genomic sequence containing 3' and 5'-ends and the coding region

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gtagagaaag gcaggagggt caaacatgat tggcccggtg agaataagaa aatatcatgc      300
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gcaaggaaaa gcaccgcgga accatacgag gatatacgat cgatcaattg ctgcccctct      2640
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<210> 168
 <211> 1629

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
Genomic sequence containing the coding region

<400> 168

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<210> 169

<211> 1629

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
Coding region without introns

<400> 169

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<210> 170

<211> 542

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
Protein sequence

<400> 170

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Met Leu Asn Ala Ala Val Ala Ala Pro Arg Cys Phe Val Tyr Pro Thr
1              5              10              15

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Asp Arg Ala Ala Met Arg Leu Gly Phe Ala Leu Arg Leu Ser Ser Pro
          20              25              30

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```

Ala Pro Leu Phe Ser Thr Ala Pro Phe Arg Arg Gln Leu His Ala Ser
          35              40              45

```

```

Gly Val Arg Ser Ile Glu Pro Val Ile Phe Arg Asn Ser Leu Glu Lys
50              55              60

```

```

Thr Leu Glu Ala His Arg Ser Ser Asn Arg Ala Ser Leu Ile Arg Lys
65              70              75              80

```

```

Val Ile Asn His Asp Cys Pro Ala Glu Thr Pro Pro Pro Ile Leu Pro
          85              90              95

```

```

Leu Glu Asn Arg Ala Gly His Asp Gln Ser Ser Gln Lys Ala Ser Ser
          100              105              110

```

```

Val Ser Asn Ala Glu Ser Glu Ser Pro Arg Ser Ser Ala Pro Ala Arg
          115              120              125

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```

Arg Ala Gln Arg Lys Ala Arg Ser Pro Ser Gln Val Ala Thr Pro Gln
          130              135              140

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Pro Gln Thr Thr Glu Tyr Pro Gln Leu Gln Trp His Ala Asp Glu Thr
145              150              155              160

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Lys Gly Arg Pro Ala Gln Ser Pro Trp Leu Lys Tyr Leu Thr Thr Asp
          165              170              175

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Trp Lys Thr Pro Asp Ala Val Ser Arg Leu Asp Ala Glu Ile Arg Ala

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180										185					190						
Leu	Glu	Leu	Tyr	Met	Thr	Pro	Thr	Pro	Ser	Glu	Arg	Thr	Glu	Ile	Asp						
		195						200					205								
Arg	Leu	Val	Ala	Asp	Met	Gly	Arg	Leu	Leu	Ala	Gly	Ile	Val	Pro	Ser						
	210					215					220										
Pro	Pro	Gln	Val	Thr	Gly	Ser	Trp	Arg	Thr	Arg	Phe	Ala	Leu	Ser	His						
225					230					235					240						
Ser	Gly	Leu	Asp	Phe	Val	Leu	Pro	Val	Pro	Asp	Ser	Asp	Arg	Ser	Thr						
				245						250				255							
Arg	Asp	Val	Arg	Lys	Pro	Ser	Ala	Thr	Arg	Pro	Lys	Val	Leu	Gln	Thr						
			260					265					270								
Tyr	Lys	Lys	Leu	Leu	His	Glu	Val	Gly	His	Ala	Leu	Gln	Gln	Ser	Pro						
	275						280					285									
Ser	Phe	Ala	Glu	Arg	Val	Arg	Ile	Ile	Gly	Ser	Arg	Phe	Pro	Val	Leu						
	290					295					300										
Ser	Ala	Ile	His	Arg	Pro	Thr	Gly	Arg	Leu	Leu	Gln	Phe	His	Cys	Gly						
305					310					315					320						
Glu	Gly	Leu	Pro	Ala	Ser	Val	Glu	Tyr	Ile	Met	Asp	Tyr	Gln	Ala	Glu						
				325					330					335							
Tyr	Pro	Ser	Ile	Arg	Pro	Leu	Tyr	Val	Thr	Ala	Arg	Leu	Ile	Leu	Glu						
			340					345					350								
Ala	Arg	Gly	Arg	Tyr	Gly	Arg	Thr	Gln	Met	Ser	Ile	Glu	Ser	Asp	Ala						
		355					360					365									
Leu	Val	Met	Leu	Leu	Val	Ala	Phe	Leu	Lys	Met	Asn	His	Gly	Arg	Phe						
		370				375					380										
Gln	Arg	Pro	Asp	Cys	Leu	Gly	Glu	Gln	Leu	Ile	Ala	Phe	Leu	Arg	Ala						
385					390					395					400						
Tyr	Gly	Ser	Asp	Ile	Asp	Leu	Thr	Thr	Thr	Gly	Val	Ser	Val	Asp	Pro						
				405					410					415							
Pro	Ser	Trp	Phe	Asn	Ala	Ser	Thr	Val	Lys	Arg	Ala	Ser	Ala	Leu	Tyr						
			420					425					430								
Ala	Pro	Asp	Asp	Leu	Pro	Ala	His	Leu	Arg	Gly	Gln	Arg	Ser	Leu	Ile						
		435					440					445									
Ser	Leu	Lys	Arg	Thr	Ala	Ala	Ala	Arg	Arg	Asn	Leu	Pro	Ala	Ala	Ser						
		450				455					460										
Arg	Leu	Cys	Val	Gln	Asp	Pro	Thr	Asn	Tyr	Met	Asn	Asp	Leu	Gly	Arg						
465					470					475					480						
Ser	Cys	Val	Arg	Thr	Leu	Glu	Leu	Gln	His	Thr	Phe	Ser	Leu	Ala	His						
				485				490						495							
Asp	Arg	Leu	Gly	Ala	Ser	Leu	Lys	Arg	Trp	Asp	Asp	Ser	Glu	Pro	Ala						
			500					505					510								

Ala Asn Val Ser Ile Leu Thr Arg Ala Leu Gln Ala Asn Phe Ser Asp
 515 520 525

Phe Glu Asn Leu Arg Ala Lys Ser Leu Lys Leu Asn Ala Thr
 530 535 540

<210> 171
 <211> 1573
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
 Genomic sequence containing 3' and 5'-ends and the coding region

<220>
 <223> misc_feature
 <223> (683)..(683)
 <223> n is a, c, g, or t

<400> 171
 tgggtgcttag ggacctgtga gtttgtgaca caaccacccc cggaaccagg gattctccac 60
 cgcgcccccg accgaccatt ttggacttgg ttagtaagct ccagtgacca gaaagcttac 120
 cagctagctt cacttgagat atcacaagat gctttggctg gcctgccacg aggtcttgct 180
 ccatgtcaac cagcaggatt cagtctctgc ctcattctcag tccaggcgag gtttctttgc 240
 tggatcttgc ggctgatgac cctcgcgatg tgggtgtccct gtccgacaag gaagcggtga 300
 ttttgcagct ctacaatcaa atccaggaac tgggaactgga aaaggcactt cttgaacaag 360
 gtacgcgtca aatttatatt ttttctaatt ttcttttttt tgtttctctg atgtagcttc 420
 ttgggcccctc caaatctgtc agcccagggt actgattccc actagagctg gaaccggctt 480
 ctgggggacaa tctggatgag caacttgcaa tcgcagaacg tgagcttctc gaggcaaggg 540
 ccacgtacac ggctcaggaga aaggccacca gtactgtcct gatgactgat ccaacattaa 600
 aagctgttca cttgaaagct atatcacctg ttgaaagggt ttacctcctt tcagtttatg 660
 cgagcatttc aattctgcat tcncctatac taacgcttca tagagctctt ctacccttgg 720
 tcaaccggcg tgatgtgttg tctttggcac atgagaacct aatgaatgag cacaacgcga 780
 ctttgaggga actatccaat ttagaagtac aaaatctaga gctacaccag aggaatcaag 840
 agctagcgcg gcagcttctt gagtccgcga aggatgatga ttcattggaga gaagcactgg 900
 atgatgacga cctcaaggca caacttgagc agctagaggc cgatcgcaaa aagagcaaat 960
 caagatggga agtcatgaaa agcgttgcaa gtgctattgt tgtgggaagt ggagtgaact 1020
 gggctgaaga cgatgagctt acagctctag tcattgatga atctgatgat taaataatcg 1080
 cctcgaaatt aatgatattcg aacaatttgg tagtattgac ttctccgacc ggcgtactac 1140
 aggatatgac ttccatttat gactagtaga gtaaacctca ttcattatatt ccaactaggg 1200
 cggatatatac acagtatcgt cttggtcgaa tcagcagaac ggctgaggaa gctcgggttag 1260
 gtaccgtaag tgcgcgccag actgccgata acctgaagac gcgccagcgc ccactagaac 1320
 aatcttcagt ggccgtgaga cccacgtgac atcatcgtcc atccacacta acaagacttg 1380
 actgtcagac catatgatatt ctgctgggtg tcccaaataa taatcttcat acatacattg 1440
 gccctgaagc cctggaatca tggagaaaat tcgaatacag atggaaggca attagaaccc 1500
 gataagggtg gcgctaattg atggatgcgt ctaagaatgt tatgcattaa tcagcgattt 1560
 acgggtaacc atg 1573

<210> 172
 <211> 573
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
 Genomic sequence containing the coding region

<220>
 <223> misc_feature
 <223> (183)..(183)
 <223> n is a, c, g, or t

<400> 172
 caacttgcaa tcgcagaacg tgagcttctc gaggcaaggg ccacgtacac ggtcaggaga 60
 aaggccacca gtactgtcct gatgactgat ccaacattaa aagctgttca cttgaaagct 120
 atatcacctg ttgaaagggt ttacctcctt tcagtttatg cgagcatttc aattctgcat 180
 tcncctatac taacgcttca tagagctctt ctacccctgg tcaaccggcg tgatgtgttg 240
 tctttggcac atgagaacct aatgaatgcg cacaacgcga ctttgaggga actatccaat 300
 ttagaagtac aaaatctaga gctacaccag aggaatcaag agctagcgcg gcagcttctt 360
 gagtccgcga aggatgatga ttcattggaga gaagcactgg atgatgacga cctcaaggca 420
 caacttgagc agctagaggc cgatcgcaaa aagagcaaat caagatggga agtcatgaaa 480
 agcgttgcaa gtgctattgt tgtgggaagt ggagtgaact gggctgaaga cgatgagctt 540
 acagctctag tcattgatga atctgatgat taa 573

<210> 173
 <211> 573
 <212> DNA
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
 Coding region without introns

<220>
 <223> misc_feature
 <223> (183)..(183)
 <223> n is a, c, g, or t

<400> 173
 caacttgcaa tcgcagaacg tgagcttctc gaggcaaggg ccacgtacac ggtcaggaga 60
 aaggccacca gtactgtcct gatgactgat ccaacattaa aagctgttca cttgaaagct 120
 atatcacctg ttgaaagggt ttacctcctt tcagtttatg cgagcatttc aattctgcat 180
 tcncctatac taacgcttca tagagctctt ctacccctgg tcaaccggcg tgatgtgttg 240
 tctttggcac atgagaacct aatgaatgcg cacaacgcga ctttgaggga actatccaat 300
 ttagaagtac aaaatctaga gctacaccag aggaatcaag agctagcgcg gcagcttctt 360
 gagtccgcga aggatgatga ttcattggaga gaagcactgg atgatgacga cctcaaggca 420
 caacttgagc agctagaggc cgatcgcaaa aagagcaaat caagatggga agtcatgaaa 480
 agcgttgcaa gtgctattgt tgtgggaagt ggagtgaact gggctgaaga cgatgagctt 540
 acagctctag tcattgatga atctgatgat taa 573

<210> 174
 <211> 190
 <212> PRT
 <213> *Aspergillus fumigatus*

<220>
 <223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381
 Protein sequence

<400> 174

Gln Leu Ala Ile Ala Glu Arg Glu Leu Leu Glu Ala Arg Ala Thr Tyr
 1 5 10 15

Thr Val Arg Arg Lys Ala Thr Ser Thr Val Leu Met Thr Asp Pro Thr
 20 25 30

Leu Lys Ala Val His Leu Lys Ala Ile Ser Pro Val Glu Arg Phe Tyr
 35 40 45
 Leu Leu Ser Val Tyr Ala Ser Ile Ser Ile Leu His Ser Pro Ile Leu
 50 55 60
 Thr Leu His Arg Ala Leu Leu Pro Leu Val Asn Arg Arg Asp Val Leu
 65 70 75 80
 Ser Leu Ala His Glu Asn Leu Met Asn Ala His Asn Ala Thr Leu Arg
 85 90 95
 Glu Leu Ser Asn Leu Glu Val Gln Asn Leu Glu Leu His Gln Arg Asn
 100 105 110
 Gln Glu Leu Ala Arg Gln Leu Leu Glu Ser Ala Lys Asp Asp Asp Ser
 115 120 125
 Trp Arg Glu Ala Leu Asp Asp Asp Asp Leu Lys Ala Gln Leu Glu Gln
 130 135 140
 Leu Glu Ala Asp Arg Lys Lys Ser Lys Ser Arg Trp Glu Val Met Lys
 145 150 155 160
 Ser Val Ala Ser Ala Ile Val Val Gly Ser Gly Val Asn Trp Ala Glu
 165 170 175
 Asp Asp Glu Leu Thr Ala Leu Val Ile Asp Glu Ser Asp Asp
 180 185 190

<210> 175

<211> 2593

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 175

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gtccactaag	aatcagaaaa	actgagcgag	tggacaaaaa	cgggtgatac	gcatacgataa	120
gcttcgactg	gaaattcgga	gatacgccata	tatttgagtt	atgtaagcac	cgccgcaggc	180
gtctcattgg	gctggggaag	ctatcaacaa	ccaccagag	cttcttgaac	ttaactccgg	240
gggtgcatga	ctaatagttt	caataatgga	cgtcggatgc	tttgtaaatac	aacggcggtc	300
ctacaatggg	gatctatgca	cagttcggtta	cataggtaaa	gttgagggca	ccaccggcga	360
gtggctcgga	gtggaatggg	atgacccac	gcgggggaag	cattctggag	aacacaacgg	420
agtgagatat	tttacaatgta	tgaaagtatt	ttcaagactg	gatagagcgg	attgactgac	480
ttgaacggaa	ggtagaagga	aacacccac	ggctgggttcg	ttcgtgcgcc	cttcgcgacg	540
gaccgacaga	cctcgaggct	tccttgaggc	agtgcgtcac	aagtatgctt	ctgagttcca	600
agaagaactc	gcaagacagc	agtcaggcga	agtctctgct	gcgcgggaaa	tcatacaaat	660
tagtagcaaa	gtagtggaag	aggtcggctt	cgacaagatc	cggaagaaac	ttgcagagct	720
ccaggaattg	aaaatcgtgc	tcctggatcg	cctatgcatc	gcaggagttc	tcctcatag	780
agcgagtcta	catgagcttg	cagaggcttg	caaggagata	gaacagacat	gtcctaagat	840
cgttgacctc	gatctgagtt	acaacttact	ggaaagctgg	gttgacattg	caaacatatg	900
tcaacagctg	aagcgcttga	agacattgaa	gctgatgttg	gtcattcagt	acatctgtga	960
gaagcatgct	gacagttggc	agcggaaatc	gtctaggtcc	tcgacaggag	ggctctgatat	1020
tcgacggtat	cacaacacta	cacttgagcg	agactctact	cgaatgggac	gaggtatgct	1080
gcacaaagct	actgcttggt	taccagtga	ctgactgact	cttggtcccc	tttagatttc	1140
agctttgaca	tatcaattcc	cgctactctc	tgctctgtct	gcctccgcaa	atcagattac	1200

ccagatcttg	acacctatca	cggataccat	cacgaccttg	acactggaaa	acaatgacat	1260
ctcttcgcta	tcttcattag	catgtctgac	ctctttgagc	aagctcgagc	acctctcgct	1320
gagagagaat	cgtatcgga	aagtctatgc	gtctggcatg	gaaggaaact	ctcttcagtt	1380
ttccgaaaat	ctcagatcgg	tggacctatc	cagaaacaat	atcgattctt	ggctgtttgt	1440
gaatgaactt	caacgcgtat	ttctgggct	gcaatctttg	cgcatatcag	gaaatcccct	1500
gtacgacaag	cctgttgccc	cctcgaacgt	cacaaattta	ccggagaagc	caatgacggt	1560
ggacgaggcc	tatatgctaa	cactctctcg	actcgcttcc	atccaaacgc	tcaactacag	1620
caagataact	tcccaagacc	gaagtaatgg	cgaactctat	tacctttccc	tcattggcaa	1680
ggagttatcc	gcgtatccgg	aaagcgcaga	acgcgagatt	cttgctacac	atccccgcta	1740
tcaggagctt	tgtgagaaat	acggagcgcc	cacaatcagg	agagccgagc	tggcaggcgc	1800
tgccgtgaat	ccgcgctctg	ttgccgccc	agtagtgaag	ttggcttttt	gcttgcactc	1860
atcagttagt	tccggtgcaa	accaagaaca	atttcgagtt	cagaagatcc	cgagatcctt	1920
taatacatat	caagtcaagg	caatcgcttc	ccgcctgttc	aatttgccgc	cttaccagtg	1980
ccgactagtc	tgggagacca	acgagttaga	ccctattcat	caggagaaaa	aggacgatgg	2040
agacgattgg	gatagtgatg	aggatgaagc	cacagctatt	ggattggggg	agagtaacaa	2100
gctcacaccg	gcgacggagg	atggaaagtt	catcagaaga	gaggttgagc	tcctggattc	2160
aacgcgagac	ataggctttt	ggttccaacc	cgatactgtt	gaggcaagga	tcagagtaga	2220
agttgcaaca	tcgaattgac	aactatttcg	acataggagt	tgtgaaggag	ttccttaacc	2280
tacattgtcg	cgggtggggg	aatatatata	gttgagcacg	actcgtgcgt	taggatacaa	2340
cgaggccaac	gacagaaaag	tagaacctct	tacgcaagcg	cctgtggcct	ctgttaccgc	2400
aatggattta	gaggccttct	tggttattct	taaacaatat	gatattgtga	gtgtatatct	2460
aagctggagg	gcaacactga	ctgctgtttt	aggactaggt	cgggttttggg	tggcagatta	2520
tcaccgcaac	tgttttgtga	taacagtgat	atcatttccc	tttcatataa	caatttaata	2580
ctcagacatc	gtc					2593

<210> 176

<211> 1974

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622
Genomic sequence containing the coding region

<400> 176

atggacgtcg	gatgctttgt	aaatcaacgg	cggctcctaca	atgggggatct	atgcacagtt	60
cgttacatag	gtaaagttga	gggcaccacc	ggcgagtggc	tcggagtggg	atgggatgac	120
cccacgcggg	ggaagcattc	tggagaacac	aacggagtga	gatattttac	atgtatgaaa	180
gtattttcaa	gactggatag	agcggattga	ctgacttgaa	cggaaggtag	aaggaaacac	240
cccacggctg	gttcgttcgt	gcgcccttcg	cgacggaccg	acagacctcg	aggcttcctt	300
gaggcagtgc	gtcacaagta	tgcttctgag	ttccaagaag	aactcgcaag	acagcagtca	360
ggcgaagtct	ctgctgcgcg	ggaaatcatc	aaatttagta	gcaaagtagt	ggaagaggtc	420
ggcttcgaca	agatccggaa	gaaacttgca	gagctccagg	aattgaaaat	cgtgctcctg	480
gatcgccatg	gcacgcgagg	agttctccct	catagagcga	gtctacatga	gcttgacagag	540
gcttgcaagg	agatagaaca	gacatgtcct	aagatcgttg	acctcgatct	gagttacaac	600
ttactggaaa	gctgggttga	cattgcaaac	atatgtcaac	agctgaagcg	cttgaagaca	660
ttgaagctga	tgttggtcat	tcagtacatc	tgtgagaagc	atgctgacag	ttggcagcgg	720
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gtgagctgac	tgactcttgg	tcccccttag	atttcagctt	tgacatatca	attcccgtca	900
ctctctgctc	tgtctgcctc	cgcaaatcag	attaccacca	tcttgacacc	tatcacggat	960
accatcacga	ccttgacact	ggaaaacaat	gacatctctt	cgctatcctc	attagcatgt	1020
ctgacctctt	tgaagaaagt	cgagcacctc	tcgctgagag	agaatcgtat	cgggaaagtc	1080
tatgcgtctg	gcatggaagg	aaactctctt	cagttttccg	aaaatctcag	atcgggtggac	1140
ctatccagaa	acaatatcga	ttcttggtcg	tttgtgaatg	aacttcaacg	cgtatttccct	1200
gggctgcaat	ctttgcgcgt	atcaggaaat	cccctgtacg	acaagcctgt	tgccccctcg	1260
aacgtcacaa	atttaccgga	gaagccaatg	acggtggacg	aggcctatat	gctaacactc	1320
tctcgactcg	cttccatcca	aacgctcaac	tacagcaaga	taacttccca	agaccgaagt	1380
aatggcgaac	tctattacct	ttccctcatt	ggcaaggagt	tatccgcgta	tccggaaagc	1440
gcagaacgcg	agattcttgc	tacacatccc	cgctatcagg	agctttgtga	gaaatacggg	1500

gcgcccacaa	tcaggagagc	cgagctggca	ggcgctgccg	tgaatccgcg	ctctgttgcc	1560
gcccagtag	tgaagttggc	tttttgcttg	cactcatcag	ttagttcccg	tgcaaaccac	1620
gaacaatttc	gagttcagaa	gatcccagaa	tcctttaata	catatcaagt	caaggcaatc	1680
gcctcccgcc	tggtcaattt	gccgccttac	cagtgccgac	tagtctggga	gaccaacgag	1740
ttagacccta	ttcatcagga	gaaaaaggac	gatggagacg	attgggatat	tgatgaggat	1800
gaagccacag	ctattggatt	gggggagagt	aacaagctca	caccggcgac	ggaggatgga	1860
aagttcatca	gaagagaggt	tgagctcctg	gattcaacgc	gagacatagg	cttttggttc	1920
caaccgata	ctgttgaggc	aaggatcaga	gtagaagttg	caacatcgaa	ttga	1974

<210> 177

<211> 1830

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622
Coding region without introns

<400> 177

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cgttacatag	gtaaagttga	gggcaccacc	ggcgagtggc	tcggagtggg	atgggatgac	120
cccacgcggg	ggaagcattc	tggagaacac	aacggagtga	gatattttac	atgtagaagg	180
aaacacccca	cggtctgttc	gttcgtgctc	ccttcgcgac	ggaccgacag	acctcgaggc	240
ttccttgagg	cagtgcgtca	caagtatgct	tctgagttcc	aagaagaact	cgcaagacag	300
cagtcaggcg	aagtctctgc	tgcgcgggaa	atcatcaaata	ttagtagcaa	agtagtgga	360
gaggtcggct	tcgacaagat	ccggaagaaa	cttgacagagc	tccaggaatt	gaaaatcgtg	420
ctcctggatc	gcctatgcat	cgcaggagtt	ctccctcata	gagcgagtct	acatgagctt	480
gcagaggctt	gcaaggagat	agaacagaca	tgctctaaga	tcgttgacct	cgatctgagt	540
tacaacttac	tggaaagctg	ggttgacatt	gcaaacatat	gtcaacagct	gaagcgcttg	600
aagacattga	agctgatgtt	ggtcattcag	tacatctgtg	agaagcatgc	tgacagttgg	660
cagcggaat	cgtctagggtc	ctcgacagga	gggtctgata	ttcgacggta	tcacaacact	720
acacttgagc	gagactctac	tcgaatggga	cgaggtatgc	tgcaaaaagc	tactgcttgg	780
ttaccaatta	cccagatctt	gacacctatc	acggatacca	tcacgacctt	gacactggaa	840
aacaatgaca	tctcttcgct	atcctcatta	gcatgtctga	cctctttgag	caagctcgag	900
cacctctcgc	tgagagagaa	tcgtatcggg	aaagtctatg	cgtctggcat	ggaaggaaac	960
tctcttcagt	tttccgaaaa	tctcagatcg	gtggacctat	ccagaaacaa	tatcgattct	1020
tggctgtttg	tgaatgaact	tcaacgcgta	tttctctggc	tgcaatcttt	gcgcataatca	1080
ggaaatcccc	tgtacgacaa	gcctgttgcc	ccctcgaacg	tcacaaatct	accggagaag	1140
ccaatgacgg	tggacgaggc	ctatatgcta	acactctctc	gactcgcttc	catccaaacg	1200
ctcaactaca	gcaagataac	ttcccaagac	cgaagtaatg	gcgaactcta	ttacctttcc	1260
ctcattggca	aggagttatc	cgcgtatccg	gaaagcgcag	aacgcgagat	tcttgctaca	1320
catccccgct	atcaggagct	ttgtgagaaa	tacggagcgc	ccacaatcag	gagagccgag	1380
ctggcaggcg	ctgccgtgaa	tccgcgctct	gttgccgccc	gagtagtgaa	gttggttttt	1440
tgcttgcaat	catcagttag	ttccggtgca	aaccaagaac	aattttcgagt	tcagaagatc	1500
ccgagatcct	ttaatacata	tcaagtcaag	gcaatcgctt	cccgcctgtt	caatttgccg	1560
ccttaccagt	gccgactagt	ctgggagacc	aacgagttag	accctattca	tcaggagaaa	1620
aaggacgatg	gagacgattg	ggatagtgat	gaggatgaag	ccacagctat	tggattgggg	1680
gagagtaaca	agctcacacc	ggcgacggag	gatggaaaag	tcatacagaag	agaggttgag	1740
ctcctggatt	caacgcgaga	cataggcttt	tggttccaac	ccgatactgt	tgaggcaagg	1800
atcagagtag	aagttgcaac	atcgaattga				1830

<210> 178

<211> 609

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622

Protein sequence

<400> 178

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Met Asp Val Gly Cys Phe Val Asn Gln Arg Arg Ser Tyr Asn Gly Asp
1      5      10      15
Leu Cys Thr Val Arg Tyr Ile Gly Lys Val Glu Gly Thr Thr Gly Glu
20      25      30
Trp Leu Gly Val Glu Trp Asp Asp Pro Thr Arg Gly Lys His Ser Gly
35      40      45
Glu His Asn Gly Val Arg Tyr Phe Thr Cys Arg Arg Lys His Pro Thr
50      55      60
Ala Gly Ser Phe Val Arg Pro Ser Arg Arg Thr Asp Arg Pro Arg Gly
65      70      75      80
Phe Leu Glu Ala Val Arg His Lys Tyr Ala Ser Glu Phe Gln Glu Glu
85      90      95
Leu Ala Arg Gln Gln Ser Gly Glu Val Ser Ala Ala Arg Glu Ile Ile
100     105     110
Lys Phe Ser Ser Lys Val Val Glu Glu Val Gly Phe Asp Lys Ile Arg
115     120     125
Lys Lys Leu Ala Glu Leu Gln Glu Leu Lys Ile Val Leu Leu Asp Arg
130     135     140
Leu Cys Ile Ala Gly Val Leu Pro His Arg Ala Ser Leu His Glu Leu
145     150     155     160
Ala Glu Ala Cys Lys Glu Ile Glu Gln Thr Cys Pro Lys Ile Val Asp
165     170     175
Leu Asp Leu Ser Tyr Asn Leu Leu Glu Ser Trp Val Asp Ile Ala Asn
180     185     190
Ile Cys Gln Gln Leu Lys Arg Leu Lys Thr Leu Lys Leu Met Leu Val
195     200     205
Ile Gln Tyr Ile Cys Glu Lys His Ala Asp Ser Trp Gln Arg Lys Ser
210     215     220
Ser Arg Ser Ser Thr Gly Gly Ser Asp Ile Arg Arg Tyr His Asn Thr
225     230     235     240
Thr Leu Gly Arg Asp Ser Thr Arg Met Gly Arg Gly Met Leu His Lys
245     250     255
Ala Thr Ala Trp Leu Pro Ile Thr Gln Ile Leu Thr Pro Ile Thr Asp
260     265     270
Thr Ile Thr Thr Leu Thr Leu Glu Asn Asn Asp Ile Ser Ser Leu Ser
275     280     285
Ser Leu Ala Cys Leu Thr Ser Leu Ser Lys Leu Glu His Leu Ser Leu
290     295     300

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Arg Glu Asn Arg Ile Gly Lys Val Tyr Ala Ser Gly Met Glu Gly Asn
 305 310 315 320
 Ser Leu Gln Phe Ser Glu Asn Leu Arg Ser Val Asp Leu Ser Arg Asn
 325 330 335
 Asn Ile Asp Ser Trp Leu Phe Val Asn Glu Leu Gln Arg Val Phe Pro
 340 345 350
 Gly Leu Gln Ser Leu Arg Ile Ser Gly Asn Pro Leu Tyr Asp Lys Pro
 355 360 365
 Val Ala Pro Ser Asn Val Thr Asn Leu Pro Glu Lys Pro Met Thr Val
 370 375 380
 Asp Glu Ala Tyr Met Leu Thr Leu Ser Arg Leu Ala Ser Ile Gln Thr
 385 390 395 400
 Leu Asn Tyr Ser Lys Ile Thr Ser Gln Asp Arg Ser Asn Gly Glu Leu
 405 410 415
 Tyr Tyr Leu Ser Leu Ile Gly Lys Glu Leu Ser Ala Tyr Pro Glu Ser
 420 425 430
 Ala Glu Arg Glu Ile Leu Ala Thr His Pro Arg Tyr Gln Glu Leu Cys
 435 440 445
 Glu Lys Tyr Gly Ala Pro Thr Ile Arg Arg Ala Glu Leu Ala Gly Ala
 450 455 460
 Ala Val Asn Pro Arg Ser Val Ala Ala Arg Val Val Lys Leu Ala Phe
 465 470 475 480
 Cys Leu His Ser Ser Val Ser Ser Gly Ala Asn Gln Glu Gln Phe Arg
 485 490 495
 Val Gln Lys Ile Pro Arg Ser Phe Asn Thr Tyr Gln Val Lys Ala Ile
 500 505 510
 Ala Ser Arg Leu Phe Asn Leu Pro Pro Tyr Gln Cys Arg Leu Val Trp
 515 520 525
 Glu Thr Asn Glu Leu Asp Pro Ile His Gln Glu Lys Lys Asp Asp Gly
 530 535 540
 Asp Asp Trp Asp Ser Asp Glu Asp Glu Ala Thr Ala Ile Gly Leu Gly
 545 550 555 560
 Glu Ser Asn Lys Leu Thr Pro Ala Thr Glu Asp Gly Lys Phe Ile Arg
 565 570 575
 Arg Glu Val Glu Leu Leu Asp Ser Thr Arg Asp Ile Gly Phe Trp Phe
 580 585 590
 Gln Pro Asp Thr Val Glu Ala Arg Ile Arg Val Glu Val Ala Thr Ser
 595 600 605
 Asn

<210> 179

<211> 1867

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 179

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taatatatat	agttgagcac	gactcgtgcg	ttaggataca	acgaggtcaa	cgacagaaaa	120
gtagaacctc	ttacgcaagc	gcctgtggcc	tctgttacct	gaatggattt	agaggccttc	180
ttggttattc	ttaaacaata	tgatatgtgt	agtgtatatt	caagctggag	ggcaaacactg	240
actgctgttt	taggactagg	tcggtttttg	gtggcagatt	atcaccgcaa	ctgtttttgtg	300
ataacagtga	tatcatttcc	ctttcatata	acaattttaat	actcagacat	cgtcattggca	360
gaatactgga	aatcagctgt	aagtgccttt	cattcagttc	cgcagacttc	ttcgtgataa	420
tctttacgtg	gggaagtccg	gcatcaactg	acagcaatat	tctagccccg	gttctgggtgc	480
aaacaatgca	agatattcat	tcgggataca	cccttcgaga	aaacccagca	tgaagcgagt	540
gccaaacacc	agggaaacct	taagcgtttc	ctacgagata	tccaccggga	aaatgaacgg	600
aagcaaaagag	aaactcagaa	ggcgaaaggat	gaagtgcagc	gattaaggca	aactgtcgca	660
ggaaaaccag	gtgcaaaaga	cagcggcgca	acagcttggg	aacacgcctc	ggctgcccct	720
ccaccggcag	aacgacctgt	gtccctggaa	gagagaaaga	agcagatagc	gcagctggca	780
gagatgggaa	ttgctatccc	ggacgaatac	cgtggtgaac	tcgcgctcgc	tggcgaatgg	840
cagacgggat	ccgaacgagt	tattcgacca	gatgacgata	cagaggaagg	aaagcctggt	900
agctctatcg	gcgttcggaa	acgcaagatg	gaaggcgatg	aggaggagca	ggaggcgcca	960
caggaggccg	agagattcgt	gagtcagggt	tggggctcga	ggactcggca	gtatcctggg	1020
gagcagagcg	atgcagacct	ggatgcactt	ctaaattcta	ccaaggatgt	aaagaaggtc	1080
aagttgtcgg	cgccggatga	agggtcgaaa	gagaaggcta	gcaaagaggg	tgctacacca	1140
agcaacgata	cggaccaggc	tgcggtcag	gagtcagaac	taccatcagt	caagtctgag	1200
ggtaaaagaag	cggcgagct	tgctacaaca	gataccccag	cggatgaagca	ggaagaggag	1260
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aatttgcagc	tgctggatat	ctattatcta	ccatgcgcac	aaatgtacag	atgatgcggt	1380
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ccgtcgccga	agcaaccag	ctcatagaag	atctggattc	tcgattcgct	tgccgagaaa	1560
gcctagtctg	gtcttgcggt	agcctatata	cagattgagt	gtatcgattc	gagcttatgc	1620
gggttgctctg	ataatattct	gccttacatt	ggcagagaga	cggttgagca	catagggtgg	1680
atggagaatg	atcagttctt	acgtatgtaa	gcattgatgtc	tagctcagaa	aagagtccca	1740
tataccatgc	gactcgttgg	cagcatccac	ctcttccttt	ggagtgcgat	ctacaatagc	1800
atgcatacga	aacaaatttc	gttgacaagg	agaccagggg	cgagaagagt	aatatagcaa	1860
gccagct						1867

<210> 180

<211> 963

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
 Genomic sequence containing the coding region

<400> 180

atggcagaat	actggaaatc	agctgtaagt	gcccttcatt	cagttccgca	gacttcttcg	60
tgataatctt	tacgtgggga	agtccggcat	caactgacag	caatattcta	gccccgggtc	120
tggtgcaaac	aatgcaagat	attcattcgg	gatacacctt	tcgagaaaac	ccagcatgaa	180
gcgagtgcc	aacaccagg	aaaccttaag	cgtttcctac	gagatatcca	ccgggaaaat	240
gaacggaagc	aaagagaaac	tcagaaggcg	aaggatgaag	tcgagcgatt	aaggcaaaact	300
gtcgcaggaa	aaccagggtc	aaaagacagc	ggcgcaacag	cttggaaca	cgctcgggt	360
gcccctccac	cggcagaacg	acctgtgtcc	ctggaagaga	gaaagaagca	gatagcgag	420
ctggcagaga	tgggaattgc	tatcccggac	gaataaccgtg	gtgaactcgc	gctcgtggc	480

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gaatggcaga cggatatccga acgagttatt cgaccagatg acgatacaga ggaaggaaag 540
cctggtagct ctatcggcgt tcggaaacgc aagatggaag gcgatgagga ggagcaggag 600
gcgcgacagg aggccgagag attcgtgagt caggggttggg gctcgaggac tcggcagtat 660
cctggggagc agagcgatgc agacctggat gcactttctaa attctaccaa ggatgtaaag 720
aaggtcaagt tgtcggcgcc ggatgaaggg tcgaaagaga aggctagcaa agaggggtgct 780
acaccaagca acgatacggg ccaggctgcg gctcaggagt cagaactacc atcagtcaag 840
tctgagggta aagaagcggc gcagcttgct acaacagata ccccgcggt gaagcaggaa 900
gaggaggcgg cacctacagg agttgttttt aagaagcgca agccgaaggt cctgaggaaa 960
tag

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<210> 181

<211> 876

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
Coding region without introns

<400> 181

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cgggatacac ctttcgagaa aaccagcat gaagcgagtg ccaaacacca gggaaacctt 120
aagcgtttcc tacgagatat ccaccgggaa aatgaacgga agcaaagaga aactcagaag 180
gcgaaggatg aagtcgagcg attaaggcaa actgtcgag gaaaaccagg tgcaaaagac 240
agcggcgcaa cagcttggaa acacgcctcg gctgcccctc caccggcaga acgacctgtg 300
tccctggaag agagaaagaa gcagatagcg cagctggcag agatgggaat tgctatcccg 360
gacgaatacc gtggtgaact cgcgctcgct ggcgaatggc agacggtatc cgaacgagtt 420
attcgaccag atgacgatac agaggaagga aagcctggta gctctatcgg cgttcggaaa 480
cgcaagatgg aaggcgatga ggaggagcag gaggcgcgac aggaggccga gagattcgtg 540
agtcagggtt ggggctcgag gactcggcag tctcctgggg agcagagcga tgcagacctg 600
gatgcacttc taaattctac caaggatgta aagaaggtca agttgtcggc gccggatgaa 660
gggtcgaaaag agaaggctag caaagagggt gctacaccaa gcaacgatac ggaccaggct 720
gcggtcagg agtcagaact accatcagtc aagtctgagg gtaaaagaagc ggcgagctt 780
gctacaacag ataccccagc ggtgaagcag gaagaggagg cggcacctac aggagttggt 840
ttaagaagc gcaagccgaa ggtcctgagg aaatag 876

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<210> 182

<211> 291

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135
Protein sequence

<400> 182

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Met Ala Glu Tyr Trp Lys Ser Ala Pro Arg Phe Trp Cys Lys Gln Cys
1           5           10           15

Lys Ile Phe Ile Arg Asp Thr Pro Phe Glu Lys Thr Gln His Glu Ala
20           25           30

Ser Ala Lys His Gln Gly Asn Leu Lys Arg Phe Leu Arg Asp Ile His
35           40           45

Arg Glu Asn Glu Arg Lys Gln Arg Glu Thr Gln Lys Ala Lys Asp Glu
50           55           60

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Val Glu Arg Leu Arg Gln Thr Val Ala Gly Lys Pro Gly Ala Lys Asp
 65 70 75 80
 Ser Gly Ala Thr Ala Trp Lys His Ala Ser Ala Ala Pro Pro Pro Ala
 85 90 95
 Glu Arg Pro Val Ser Leu Glu Glu Arg Lys Lys Gln Ile Ala Gln Leu
 100 105 110
 Ala Glu Met Gly Ile Ala Ile Pro Asp Glu Tyr Arg Gly Glu Leu Ala
 115 120 125
 Leu Ala Gly Glu Trp Gln Thr Val Ser Glu Arg Val Ile Arg Pro Asp
 130 135 140
 Asp Asp Thr Glu Glu Gly Lys Pro Gly Ser Ser Ile Gly Val Arg Lys
 145 150 155 160
 Arg Lys Met Glu Gly Asp Glu Glu Glu Gln Glu Ala Arg Gln Glu Ala
 165 170 175
 Glu Arg Phe Val Ser Gln Gly Trp Gly Ser Arg Thr Arg Gln Tyr Pro
 180 185 190
 Gly Glu Gln Ser Asp Ala Asp Leu Asp Ala Leu Leu Asn Ser Thr Lys
 195 200 205
 Asp Val Lys Lys Val Lys Leu Ser Ala Pro Asp Glu Gly Ser Lys Glu
 210 215 220
 Lys Ala Ser Lys Glu Gly Ala Thr Pro Ser Asn Asp Thr Asp Gln Ala
 225 230 235 240
 Ala Ala Gln Glu Ser Glu Leu Pro Ser Val Lys Ser Glu Gly Lys Glu
 245 250 255
 Ala Ala Gln Leu Ala Thr Thr Asp Thr Pro Ala Val Lys Gln Glu Glu
 260 265 270
 Glu Ala Ala Pro Thr Gly Val Val Phe Lys Lys Arg Lys Pro Lys Val
 275 280 285
 Leu Arg Lys
 290

<210> 183

<211> 2193

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 183

gagcaactgc	cagaaatcca	gacgtgcaac	tcctccgcaa	aaaaaagcgt	tgtctcccaa	60
aacggaggct	gttaagttat	cgccacgggg	aaatagccca	aaaggaactc	gtcacagctg	120
gaatcaacac	caagtaccga	agaaacaagc	gagcagcggc	tgtttggtt	ctgcagctgc	180
acaaaaaatg	ggaacgaagt	gaatgaggtt	agatagagat	gaggatggat	caagaagcgc	240
cctccagatg	tagcaatgaa	gagatgatgt	tgcaagaaga	ggtgaaacaa	gctggcggca	300

cgggatcagg	ctaggctaga	tagggttagc	aacgaggggtg	acatcacgtg	agaacgggca	360
togtgatatg	gatgacaatt	aacatcataa	acactcttcg	ttcagttgct	gtgactcctg	420
acgcgtaagg	ggatctgggg	tgaagtcaag	caatagactc	tctgacagat	ttgactttag	480
agaaaagtaaa	taacaccact	atggacatct	cgcaagaaac	cgttgataaa	atacgacgtt	540
tcgcgcaaaa	gcgcaaaaa	gcggaggagt	tctacgagga	acactcggta	aatccagcta	600
attttgacgc	ttacaatcgc	aagttggatg	agacgttggc	agagctgcag	gctcaagtca	660
aacgtcatga	ggatgagctc	cgcaaggtag	gtcaacaagt	tgcctagaat	ataagccgac	720
tgtcacaaga	gatttcatgc	atgaattagg	aatactgaca	agaggaaacag	ctacgcatga	780
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gcagagccaa	gaaagcgtat	gattctcttc	tgcaatcgga	aacgcgactg	ccgagtcag	900
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ggctgaacgc	agaaaaatcg	agtcaagtc	agaaaactcc	tgcgacagctt	gcgtatgatc	1140
tcgtcaagga	gcagcaggaa	aagatcgaga	gacttgatac	taccacagaa	gagctaaagt	1200
cctctctcta	taaatttgtc	gaagacacac	ttgcccacat	gcttgctgca	gaaaatctgg	1260
gcggtccac	tgtcggagat	gcgttgga	tttcggacac	taccttaaaa	gcgggctaca	1320
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aacagcggat	tgacgagctt	gttcgtcgcc	aaactgcgca	ggagggcaac	gagcaggcaa	1440
cccttttgaa	caaaagagag	gcggccgcgcg	ctgaaatgcg	agctcttctt	actgctctgt	1500
tagatgcgga	ttactcctat	gtcgaccttc	cgacagagtc	agcggcctcg	cgctttctag	1560
taagagcgaa	ggtagctcaa	ttccatccgc	gcgatgccag	gaagcttcgg	ttaattgatt	1620
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aatggtatc	acatttcacc	aaacatctgg	gaaaagacaa	acagacgcca	tccccacgga	1740
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caacgaagaa	gcggccccga	aagccactgg	tagcataacg	ccttgagaat	gcgagagata	1860
catcaaaagc	ttatcagaaa	gttcaatgct	cgaggtcaaa	aatataccgt	taatgccata	1920
caagaaacat	ggaagaagaa	agaccgtagc	cggttatcag	atcggcatca	ttccgatgct	1980
ggtagaagta	ctcttgccg	tattctttgc	tttgagacca	gttcgggaac	ccgccgagcg	2040
cttggtgact	tgatcgctgg	gctcccttct	aggtcgcggc	gtttttattt	ttgaactcga	2100
ccctgtagcg	ttcttgccgt	ggaagcgctt	cttgacgaa	gtctttcttt	tcttggaacg	2160
gctagtctcg	gtgtcttcat	actcttcgga	tga			2193

<210> 184

<211> 1448

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
 Genomic sequence containing the coding region

<400> 184

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ggaaacgagt	cggagaccta	tacggatgcc	aaggctgagc	cttccgctgc	gccaagtgc	180
actgctgatg	gccaggcgga	cactgttgtt	cctgatgctc	caaatggtaa	gggtgcatcc	240
acggagacgc	agccaattca	gtcgaccgcg	tctcatggcg	agcgcgtac	ttctcagccc	300
gaacagcagc	gcccacaaga	tgaatccagc	tggattcaca	ttcgcgctgt	aatttctagc	360
caggaaagctg	ccacagtcac	tggcaagggt	ggagaaaaacg	tatctcagat	tcgtcgtttg	420
tctggagcaa	agtgcactgt	cagcgactac	tcccgtgggtg	cagtcgaacg	tattttgacc	480
gtgagcggcc	cacaggatgc	cgttgccaag	gttggttttt	tgatctatcc	ttcgctgttt	540
gaaagattgc	taattcagag	taggcggttg	gtttgatcat	ccgtacattg	aacaatgaac	600
ctcttgatgc	cccctctacc	gcccattcca	agacataccc	tctgcgtttg	ctgatcccc	660
atctccttat	tggctccatc	attggcaaag	gtggttcacg	cattcgcgaa	attcaggaag	720
cttctggtgc	cogactgaat	gcacccgatt	cgtgccttcc	cttgctcctc	gagcggtcac	780
ttgtaattct	cggcggttgc	gattctgtcc	acatcgctac	ctaactacgtc	gccgtaaccc	840
tcgttgagca	gctcactgag	cgctttggag	gtcctgcagc	ctcagcttat	gccactcgca	900
gcggtggccc	tgctggagca	gtgcctggcg	gtatgcaggt	tgtcccgtat	gttccacagc	960
ccgctggttg	tcaatatggc	catccagaac	atttcaagag	acaccatcac	caccccaatc	1020

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gcgctgctgc aggcgcctat ggggtccctt accttcacgg tcagcctgct cccgcaccag 1080
tgccccagcc ggctttgcat tatggagctg ctccccatgc cccttacgca ggagctggcc 1140
cccatcagcc tgctccatac ggcgcaccgc agcccgctca ggcacgcggc gctcctaccc 1200
ctgccacacc cgttggaggt gtcattgcctg gtcagccatt gactcagcag atctacatcc 1260
ccaacgacat ggttgggtgcc atcatcggaa agggcggtgc gaagatcaat gagattcgac 1320
acctcagtg gctgtgtgatc aagattaatg agcctcaaga gaacagcaat gagcggtttg 1380
tgactattac tggaaaccag gaatgcaacc aaatggctct gtacatgctt tactcgcgac 1440
ttggttag

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<210> 185

<211> 1395

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
Coding region without introns

<400> 185

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ccgtccggac caaatgatca gccagaagct aaacgtcctg ccttggacaa agtagtaaag 120
ggaaacgagt cggagacctt tacggatgcc aaggctgagc cttccgctgc gccaagtgtc 180
actgctgatg gccaggggcg cactgttggt cctgatgctc caaatggtaa ggggtgcatcc 240
acggagacgc agccaattca gtcgaccgcg tctcatggcg agcgcgctac ttctcagccc 300
gaacagcagc gccacaaga tgaatccagc tggattcaca ttgcgctgt aatttctagc 360
caggaagctg ccacagtcac tggcaagggt ggagaaaacg tatctcagat tcgtcgtttg 420
tctggagcaa agtgactgt cagcgactac tccggtggtg cagtcgaacg tattttgacc 480
gtgagcggcc cacaggatgc cgttgccaag gcgtttggtt tgatcatccg tacattgaac 540
aatgaacctc ttgatgcccc ctctaccgcc caatccaaga cataccctct gcgtttgctg 600
atcccccatc tcttatttgg ctccatcatt ggcaaagggt gttcacgcac tcgcgaaatt 660
caggaagctt ctggtgcccc actgaatgca tccgattcgt gccttccctt gtctctgag 720
cggctcactt taattctcgg cgttgccgat tctgtccaca tcgctaccta ctacgtcgcc 780
gtaaccctcg ttgagcagct cactgagcgc tttggaggtc ctgcagcctc agcttatgcc 840
actcgcagcg gtggccctgc tggagcagtg cctggcggtg tgcaggttgt cccgtatgtt 900
ccacagcccc ctggtggtca atatggccat ccagaacatt tcaagagaca ccatcaccac 960
cccaatcgcg ctgctgcagg cgctatggg gtcccttacc ttcacggtca gcctgtctcc 1020
gcaccagtgg cccagccggc tttgcattat ggagctgctc cccatgcccc ttacgcagga 1080
gctggcccc atcagcctgc tccatacggc gcaccgcagc ccgctcaggc acgcggcgct 1140
cctacccctg ccacaccctg tggaggtgtc atgcctggtc agccattgac tcagcagatc 1200
tacatcccca acgacatggt tggtgccatc atcggaaagg gcggtgcgaa gatcaatgag 1260
attcgacacc tcagtggcag tgtgatcaag attaatgagc ctcaagagaa cagcaatgag 1320
cgtttggtga ctattactgg aaccagga tgcaaccaa tggctctgta catgctttac 1380
tcgcgacttg gttag

```

<210> 186

<211> 464

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663
Protein sequence

<400> 186

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Met Ser Ala Ser Pro Ser Ala Leu Gln Ser Thr Lys Arg Pro Leu Glu
1           5           10           15

```

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Asp Pro Ser Ser Pro Ser Gly Pro Asn Asp Gln Pro Glu Ala Lys Arg

```

20										25					30				
Pro	Ala	Leu	Asp	Lys	Val	Val	Lys	Gly	Asn	Glu	Ser	Glu	Thr	Tyr	Thr				
		35					40					45							
Asp	Ala	Lys	Ala	Glu	Pro	Ser	Ala	Ala	Pro	Ser	Ala	Thr	Ala	Asp	Gly				
		50				55					60								
Gln	Gly	Asp	Thr	Val	Val	Pro	Asp	Ala	Pro	Asn	Gly	Lys	Gly	Ala	Ser				
		65			70					75					80				
Thr	Glu	Thr	Gln	Pro	Ile	Gln	Ser	Thr	Ala	Ser	His	Gly	Glu	Arg	Ala				
				85					90					95					
Thr	Ser	Gln	Pro	Glu	Gln	Gln	Arg	Pro	Gln	Asp	Glu	Ser	Ser	Trp	Ile				
			100					105					110						
His	Ile	Arg	Ala	Val	Ile	Ser	Ser	Gln	Glu	Ala	Ala	Thr	Val	Ile	Gly				
		115					120					125							
Lys	Gly	Gly	Glu	Asn	Val	Ser	Gln	Ile	Arg	Arg	Leu	Ser	Gly	Ala	Lys				
		130				135					140								
Cys	Thr	Val	Ser	Asp	Tyr	Ser	Arg	Gly	Ala	Val	Glu	Arg	Ile	Leu	Thr				
		145			150					155					160				
Val	Ser	Gly	Pro	Gln	Asp	Ala	Val	Ala	Lys	Ala	Phe	Gly	Leu	Ile	Ile				
				165					170					175					
Arg	Thr	Leu	Asn	Asn	Glu	Pro	Leu	Asp	Ala	Pro	Ser	Thr	Ala	Gln	Ser				
			180					185					190						
Lys	Thr	Tyr	Pro	Leu	Arg	Leu	Leu	Ile	Pro	His	Leu	Leu	Ile	Gly	Ser				
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Ile	Ile	Gly	Lys	Gly	Gly	Ser	Arg	Ile	Arg	Glu	Ile	Gln	Glu	Ala	Ser				
		210				215					220								
Gly	Ala	Arg	Leu	Asn	Ala	Ser	Asp	Ser	Cys	Leu	Pro	Leu	Ser	Ser	Glu				
		225			230					235					240				
Arg	Ser	Leu	Val	Ile	Leu	Gly	Val	Ala	Asp	Ser	Val	His	Ile	Ala	Thr				
				245					250					255					
Tyr	Tyr	Val	Ala	Val	Thr	Leu	Val	Glu	Gln	Leu	Thr	Glu	Arg	Phe	Gly				
			260					265					270						
Gly	Pro	Ala	Ala	Ser	Ala	Tyr	Ala	Thr	Arg	Ser	Gly	Gly	Pro	Ala	Gly				
		275					280					285							
Ala	Val	Pro	Gly	Gly	Met	Gln	Val	Val	Pro	Tyr	Val	Pro	Gln	Pro	Ala				
		290				295					300								
Gly	Gly	Gln	Tyr	Gly	His	Pro	Glu	His	Phe	Lys	Arg	His	His	His	His				
		305			310					315					320				
Pro	Asn	Arg	Ala	Ala	Ala	Gly	Ala	Tyr	Gly	Val	Pro	Tyr	Leu	His	Gly				
			325						330					335					
Gln	Pro	Ala	Pro	Ala	Pro	Val	Ala	Gln	Pro	Ala	Leu	His	Tyr	Gly	Ala				
			340					345					350						

Ala Pro His Ala Pro Tyr Ala Gly Ala Gly Pro His Gln Pro Ala Pro
 355 360 365

Tyr Gly Ala Pro Gln Pro Ala Gln Ala Arg Gly Ala Pro Thr Pro Ala
 370 375 380

Thr Pro Val Gly Gly Val Met Pro Gly Gln Pro Leu Thr Gln Gln Ile
 385 390 395 400

Tyr Ile Pro Asn Asp Met Val Gly Ala Ile Ile Gly Lys Gly Gly Ala
 405 410 415

Lys Ile Asn Glu Ile Arg His Leu Ser Gly Ser Val Ile Lys Ile Asn
 420 425 430

Glu Pro Gln Glu Asn Ser Asn Glu Arg Leu Val Thr Ile Thr Gly Thr
 435 440 445

Gln Glu Cys Asn Gln Met Ala Leu Tyr Met Leu Tyr Ser Arg Leu Gly
 450 455 460

<210> 187

<211> 2121

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 187

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agtaccgaag	aaacaagcga	gcagcggtcg	tttggcttct	gcagctgcac	aaaaaatggg	120
aacgaagtga	atgaggttag	atagagatga	ggatggatca	agaagcgccc	tccagatgta	180
gcaatgaaga	gatgatgttg	caagaagagg	tgaaacaagc	tggcggcacg	ggatcaggct	240
aggctagata	gggttagcaa	cgagggtgac	atcacgtgag	aacgggcatc	gtgatatgga	300
tgacaattaa	catcataaac	actcttcggt	cagttgctgt	gactcctgac	gcgtaagggg	360
atctggggtg	aagtcaagca	atagactctc	tgacagattt	gacttttagag	aaagtaaata	420
acaccactat	ggacatctcg	caagaaaccg	ttgataaaat	acgacgtttc	gcgcaaaagc	480
gccaaaaagc	ggaggagttc	tacgaggaac	actcggtaaa	tccagctaata	tttgacgctt	540
acaatcgcaa	gttggatgag	acgttggcag	agctgcaggc	tcaagtcaaa	cgatcatgag	600
atgagctccg	caaggtagct	caacaagttg	cctagaatat	aagccgactg	tcacaagaga	660
tttcatgcat	gaattaggaa	tactgacaag	aggaacagct	acgcatgacc	accacgatcg	720
agttcgctca	aattggggca	gaccttggg	cccgcatctc	agaagtgcgc	agagccaaga	780
aagcgataga	ttctcttctg	caatcggaag	cgcgactgcc	gagtcaggcg	tcgcccctgc	840
cttcattact	tgcggttgac	gaggcgtctc	gtctcgtcaa	ggagagcaag	acctcaatct	900
cactgacggc	ggagaaaactg	tctgcggatc	gtcagcgctt	gaaagcggaa	gaagccaatt	960
tgcgcgatgc	gcaactgatc	aaagacgggt	tgagagaaaag	gattgagcgg	ctgaacgcag	1020
aaaaatcgag	tcaagtccag	aaaactcctg	cgcagcttgc	gtatgatctc	gtcaaggagc	1080
agcaggaaaa	gatcgagaga	cttgataacta	ccacagaaga	gctaaagtcc	tctctctata	1140
aatttgctga	agacacactt	gccccaatgc	ttgctgcaga	aaatctgggc	ggtcccactg	1200
tcggagatgc	ggttgaaatt	tcggacacta	ccctaaaagc	gggctacact	agccatggga	1260
agcctaagaa	accaaaaact	ccggccgtgg	ggacttctga	cagtggccaa	cagcggattg	1320
acgagcttgt	tcgtcgccaa	actgcgcagg	agggcaacga	gcaggcaacc	cttttgaaca	1380
aaagagaggc	ggccgccgct	gaaatgcgag	ctcttcttac	tgctctgtta	gatgcggatt	1440
actcctatgt	cgaccttccg	cacgagtcag	cggcctcgcg	ctttctagta	agagcgaagg	1500
tagctcaatt	ccatccgcgc	gatgccagga	agcttcgggt	aattgatttt	ggcgctcat	1560
tagtcgattg	aggtggctac	atgtaccgta	ctacatctcc	cagcttacaa	atggatatcac	1620
atttcaccaa	acatctggga	aaagacaaac	agacgccatc	cccacggata	tatagcgact	1680
caaccgaaag	ccagtaagat	atctagagcc	ggcgaaaacc	acgtgtttca	acgaagaagc	1740

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ggccccgaaa gccactggta gcataacgcc ttgagaatgc gagagataca tcaaaagctt 1800-
atcagaaaagt tcaatgctcg aggtcaaaaa tataccgtta atgccataca agaaacatgg 1860
aagaagaaaag accgtagccg ggtatcagat cggcatcatt ccgatgctgg tagaagtact 1920
cttggccgta ttctttgctt tggagccagt tcgggaaccc gccgagcgct tgttgacttg 1980
atcgctgggc tcccttctag gtcgcggcgt ttttattttt gaactcgacc ctgtagcggt 2040
cttgcggtgg aagcgcttct tggacgaagt ctttcttttc ttggaacggc tagtctcggt 2100
gtcttcatac tcttcggatg a 2121

```

<210> 188

<211> 1143

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
Genomic sequence containing the coding region

<400> 188

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gcgaggaggt tctacgagga aactcggta aatccagcta attttgacgc ttacaatcgc 120
aagttggatg agacgttggc agagctgcag gctcaagtca aacgtcatga ggatgagctc 180
cgcaaggtac gtcaacaagt tgccatagaat ataagccgac tgtcacaaga gatttcatgc 240
atgaattagg aatactgaca agaggaacag ctacgcatga ccaccacgat cgagttcgct 300
caaattgggg cagatccttg ggcccgcata tcagaagtgc gcagagccaa gaaagcgat 360
gattctcttc tgcaatcggg aacgcgactg ccgagtcag gctcgccctt gccttcatta 420
cttgcggttg acgaggcgct tcgtctcgct aaggagagca agacctcaat ctactgacg 480
gcgagaaaaa tgtctgcgga tcgtcagcgc ttgaaagcgg aagaagccaa tttgcgcgat 540
gcgcaactga tcaaagacgg gttggagaaa aggattgagc ggctgaacgc agaaaaatcg 600
agtcaagtcc agaaaactcc tgcgcagctt gcgtatgatc tcgtcaagga gcagcaggaa 660
aagatcgaga gacttgatac taccacagaa gagctaaagt cctctctcta taaatttgct 720
gaagacacac ttgcccacat gcttgctgca gaaaatctgg gcggtccac tgctcgagat 780
gcgttggaat tttcggacac taccttaaaa gcgggctaca ctagccatgg gaagcctaag 840
aaacaaaaaa ctccggccgt ggggacttct gacagtggcc aacagcggat tgacgagctt 900
gttcgtcgcc aaactgcgca ggagggaac gagcaggcaa cccttttgaa caaaagagag 960
gcggccgccc ctgaaatgct agctcttctt actgctctgt tagatgcgga ttactcctat 1020
gtcgaccttc cgcacgagtc agcggcctcg cgctttctag taagagcgaa ggtagctcaa 1080
ttccatccgc gcgatgccag gaagcttcgg ttaattgatt ttgggcgctc attagtcgat 1140
tga 1143

```

<210> 189

<211> 1035

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
Coding region without introns

<400> 189

```

atggacatct cgcaagaaac cgttgataaa atacgacgtt tcgcgcaaaa gcgcaaaaaa 60
gcgaggaggt tctacgagga aactcggta aatccagcta attttgacgc ttacaatcgc 120
aagttggatg agacgttggc agagctgcag gctcaagtca aacgtcatga ggatgagctc 180
cgcaaggtac gtcaacaagt tgccatagaat ataagccgac tgtcacaaga gatttcatgc 240
aagaagcgt atgattctct tctgcaatcg gaaacgcgac tgccgagtc aggtcgccc 300
ttgccttcat tacttgcggt tgacgaggcg tctcgtctcg tcaaggagag caagacctca 360
atctcactga cggcgagaa actgtctgct gatcgtcagc gcttgaaagc ggaagaagcc 420
aatgtgcgct atgcgcaact gatcaaagac ggggttgaga aaaggattga gcggctgaac 480
gcagaaaaat cgagtcaagt ccagaaaact cctgcgcagc ttgcgtatga tctcgtcaag 540
gagcagcagg aaaagatcga gagacttgat actaccacag aagagctaaa gtcctctctc 600

```



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tataaatttg tcgaagacac acttgcccca atgcttgctg cagaaaatct gggcggtccc 660
actgtcggag atgcgttgga aatttcggac actaccttaa aagcgggcta cactagccat 720
gggaagccta agaaaccaa aactccggcc gtggggactt ctgacagtgg ccaacagcgg 780
attgacgagc ttgttcgtcg ccaaactgcg caggagggca acgagcaggc aacccttttg 840
aacaaaagag aggcggccgc cgctgaaatg cgagctcttc ttactgctct gttagatgcg 900
gattactcct atgtcgacct tccgcacgag tcagcggcct cgcgctttct agtaagagcg 960
aaggtagctc aattccatcc gcgcgatgcc aggaagcttc ggttaattga ttttgggcgc 1020
tcattagtcg attga 1035

```

<210> 190

<211> 344

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267
Protein sequence

<400> 190

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Met Asp Ile Ser Gln Glu Thr Val Asp Lys Ile Arg Arg Phe Ala Gln
1           5           10           15

```

```

Lys Arg Gln Lys Ala Glu Glu Phe Tyr Glu Glu His Ser Val Asn Pro
20           25           30

```

```

Ala Asn Phe Asp Ala Tyr Asn Arg Lys Leu Asp Glu Thr Leu Ala Glu
35           40           45

```

```

Leu Gln Ala Gln Val Lys Arg His Glu Asp Glu Leu Arg Lys Phe Ala
50           55           60

```

```

Gln Ile Gly Ala Asp Pro Trp Ala Arg Ile Ser Glu Val Arg Arg Ala
65           70           75           80

```

```

Lys Lys Ala Tyr Asp Ser Leu Leu Gln Ser Glu Thr Arg Leu Pro Ser
85           90           95

```

```

Pro Gly Ser Pro Leu Pro Ser Leu Leu Ala Val Asp Glu Ala Ser Arg
100          105          110

```

```

Leu Val Lys Glu Ser Lys Thr Ser Ile Ser Leu Thr Ala Glu Lys Leu
115          120          125

```

```

Ser Ala Asp Arg Gln Arg Leu Lys Ala Glu Glu Ala Asn Leu Arg Asp
130          135          140

```

```

Ala Gln Leu Ile Lys Asp Gly Leu Glu Lys Arg Ile Glu Arg Leu Asn
145          150          155          160

```

```

Ala Glu Lys Ser Ser Gln Val Gln Lys Thr Pro Ala Gln Leu Ala Tyr
165          170          175

```

```

Asp Leu Val Lys Glu Gln Gln Glu Lys Ile Glu Arg Leu Asp Thr Thr
180          185          190

```

```

Thr Glu Glu Leu Lys Ser Ser Leu Tyr Lys Phe Val Glu Asp Thr Leu
195          200          205

```

```

Ala Pro Met Leu Ala Ala Glu Asn Leu Gly Gly Pro Thr Val Gly Asp
210          215          220

```

Ala Leu Glu Ile Ser Asp Thr Thr Leu Lys Ala Gly Tyr Thr Ser His
 225 230 235 240

Gly Lys Pro Lys Lys Pro Lys Thr Pro Ala Val Gly Thr Ser Asp Ser
 245 250 255

Gly Gln Gln Arg Ile Asp Glu Leu Val Arg Arg Gln Thr Ala Gln Glu
 260 265 270

Gly Asn Glu Gln Ala Thr Leu Leu Asn Lys Arg Glu Ala Ala Ala Ala
 275 280 285

Glu Met Arg Ala Leu Leu Thr Ala Leu Leu Asp Ala Asp Tyr Ser Tyr
 290 295 300

Val Asp Leu Pro His Glu Ser Ala Ala Ser Arg Phe Leu Val Arg Ala
 305 310 315 320

Lys Val Ala Gln Phe His Pro Arg Asp Ala Arg Lys Leu Arg Leu Ile
 325 330 335

Asp Phe Gly Arg Ser Leu Val Asp
 340

<210> 191

<211> 2000

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA283; clone 11-6-20; contig 4910 region 9638-11637
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 191

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tctgcaagat	cagtaattat	gtaggaacac	gaaaacaatg	ttctacacat	tagttttctc	180
ctgatgacca	tcttctcttt	gatcaatgca	gcagacaaca	aatcctgtcc	aatcatccca	240
acatactgtt	tcctaccttg	attggcgcaa	atccggcgac	aataatcaag	ggtagagtga	300
tggactaggc	tcaggcggtt	tgactttgca	aatccaattg	aattctgatc	agtgctaagc	360
cgatgatggc	gttgagcgac	caaggacaat	ttccgactga	gtcagcattt	tccctcgctc	420
gcgactcgcg	aggcgcggtc	caggacggga	ggtcttgga	aggctgaacg	gtcaatcaat	480
catcaaattg	gtaggatggt	gcgtaaatag	cccacatgcg	cataaaaagt	gatgagtgcc	540
gcacgggtat	cttcggttctt	gtttcctttt	ccgtctcacc	ccaagatcat	gggtcatgaa	600
ttgataatag	tatcgtcaac	tggcttagcg	tgatgactac	gtatcttttt	gagcgtcaag	660
ttcggctcgtt	tcaatcggag	tggttttctc	cgccaacgcc	tagtccattg	ctcccaagag	720
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aaaacgtatg	tacgaagaat	ggatcatctc	tcaaagtact	atactccgta	ctcttgcttg	840
tattctgata	tttcagttca	ataatcgaaa	aatagtgcg	cgcggtatgg	tgcagatctt	900
atgcagatag	gacagtcagc	ccgccagtat	tacggagaac	ctaaggtact	catagtaaag	960
tatgatgata	cggccgcata	cgacctctaa	ttcatcgaat	actccagaag	cggctagcca	1020
ctttcctgaa	atcgaggtct	atccatggac	tcagcatctt	gtacggagta	caaactcctg	1080
ccagcttatt	ccaactgatg	accctggccc	ttatatgagc	aagcaggata	tgattgggag	1140
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ctctcgtatg	gggtaaatca	atgcaccgga	aatttacata	tgatatcaaa	agtagtagtt	1500
ctccgactag	ggaggatgga	gcaaggtaat	ctatatattat	tggctgctcg	tttgcaggcc	1560

aaacccaaaac	caacatgctc	tgtatcttag	cctccgtatc	tgatctcata	tctttgagga	1620
cattgattgg	attgtcgatc	ccaatgacgg	cgtgctgaga	ctgttctaaa	gagagctcaa	1680
aagaaataga	gcaaaaagtaa	gatcatctac	ggactatcta	cgctctatag	gagtttcaact	1740
ctgtgataat	ggctcacgcc	cacataaact	gtccatgacg	aaatcgatac	agcctcaaga	1800
aagccaacaa	tttttagtttg	gaagtcgaat	cacaccacat	aggttaacca	gcaaaaagcgc	1860
agacctccaa	taaaggttcg	ctcatcggtc	ccttctgctg	ctactttgga	gctaaagctg	1920
cgcgtctgta	catcttgacc	tccttcggcc	tctcctttgc	gctgtgctca	gttttccctt	1980
cctttgtctc	ttggactgga					2000

<210> 192

<211> 4336

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899
region 472441-476776

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 192

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cggcaaatgc	tcgcgcaccg	accacggaa	ttcggccaag	attctggatc	gattgcccct	180
tatgtatgcg	aaggtttggg	gatgtgattg	gtgtgcagcg	taaacgagta	cggattgata	240
agagtgccaa	gatttgaacc	actgttcacg	tcattggagg	gggtttccgg	cacgccgggt	300
aggagtgaga	cagagtgcct	ttaaataatg	gcgatacccc	cgcaacgacg	ggagaagaaa	360
atctgggtct	acaacctagg	ctttaatttc	caagttgatt	tcaagtgcgt	gtgtatggac	420
tctcactcgc	ttgaagatac	gatatacatg	aagcctcctt	aggataactg	caactggaata	480
gaacattttc	gttatataac	atgggtgcgc	agaagaagca	atcctctgat	aactctcagg	540
cctttgtctc	gcctgctcat	gcgcttcgct	atgaggatgt	ccttcgtgag	ctggccgctg	600
atccagacca	gggtctgacc	gtgggggagg	cgaagcgaag	actccaacaa	tatgggtccga	660
atgaactgga	agggggagag	gggtgttcca	ttgtcaagat	tgctcattag	cagatcgcaa	720
atgcatgatg	gctggttagt	ctctcccttt	tggttagacg	acaactgacg	acaactgacg	780
acagcaggtc	ctgatcatcg	ccatggcggt	cagtttcggc	attcaatcct	ggattgaggg	840
tggtgtcatt	ggggctgtca	ttggtctaaa	cattgtggta	gggtgtctat	aagactatgc	900
cgcagagaaa	acgatggatt	cccttcgact	gttgagttct	cccaccggaa	ctgtcacgcg	960
tgatggcaaa	accagtacca	ttcctgccaa	cgagattgtc	cccggggaca	tgattgaact	1020
caaagtggga	gacacgggtc	ctgcggatct	tcggtgcgta	aagagttacc	agaaaaatct	1080
gttcccgttc	actaaccgcc	gataggctcg	ttgatgcaat	gaatttcgaa	accgacgagg	1140
ccctcctgac	tgccgagtcg	ctgccgggtg	agaaaagagg	cgataccact	tttgacccag	1200
acacgggacc	tggtgatcgg	ttgaatattg	cgtatagttc	ctccacgggtg	acgagaggcc	1260
gcgctcgggg	cgttggtatc	agcacgggga	tgcaaaccca	gattggagcc	atcgccgctg	1320
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agaagcgatg	gtacgtgcag	gcgtggaccc	tgacttgacg	ggatgccgtg	ggacgggttc	1440
tggaatcaa	cgttggcaca	ccgctgcagc	gcaaaactct	gaaactggct	ttggcccttt	1500
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<211> 3336

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899
region 472441-476776

Genomic sequence containing the coding region

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<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899
region 472441-476776

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<213> *Aspergillus fumigatus*

<220>

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899
region 472441-476776
Protein sequence

<400> 195

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 Val Lys Ile Val Ile Arg Gln Ile Ala Asn Ala Met Met Leu Val Leu
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 Gly Val Ile Gly Ala Val Ile Gly Leu Asn Ile Val Val Gly Val Tyr
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 Gln Asp Tyr Ala Ala Glu Lys Thr Met Asp Ser Leu Arg Ser Leu Ser
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 Thr Val Pro Ala Asp Leu Arg Leu Val Asp Ala Met Asn Phe Glu Thr
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 Glu Thr Lys Lys Arg Trp Tyr Val Gln Ala Trp Thr Leu Thr Cys Thr
 260 265 270
 Asp Ala Val Gly Arg Phe Leu Gly Ile Asn Val Gly Thr Pro Leu Gln
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 Arg Lys Leu Ser Lys Leu Ala Leu Ala Leu Phe Ala Ile Ala Ile Ile
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Pro	Pro	Gln	Ser	Val	Ser	Ile	Phe	Thr	Trp	Glu	Val	Ile	Val	Asp	Thr
	850					855					860				
Met	Val	Tyr	Gly	Val	Trp	Met	Ala	Ala	Leu	Cys	Leu	Ala	Ser	Phe	Ser
865					870					875					880
Leu	Val	Leu	Phe	Gly	Trp	Gly	Asp	Gly	Asn	Leu	Ala	Ser	Gly	Cys	Asn
				885					890					895	
Ser	Asp	Tyr	Ser	Pro	Glu	Cys	Asp	Gly	Val	Phe	Arg	Ala	Arg	Ala	Thr
			900					905					910		
Thr	Phe	Val	Cys	Met	Thr	Trp	Phe	Ala	Leu	Phe	Leu	Ala	Trp	Glu	Met
		915					920					925			
Ile	Asp	Met	Arg	Arg	Ser	Phe	Phe	Arg	Met	Gln	Pro	Asn	Ser	Lys	Arg
	930					935					940				
Tyr	Phe	Thr	Gln	Trp	Met	Phe	Asp	Val	Trp	Arg	Asn	Lys	Phe	Leu	Phe
945					950					955					960
Ser	Gly	Ile	Met	Ile	Gly	Phe	Val	Thr	Thr	Phe	Pro	Ile	Leu	Tyr	Ile
				965					970					975	
Pro	Val	Ile	Asn	Asp	Val	Val	Phe	Lys	His	Val	Gly	Ile	Ser	Trp	Glu
			980					985					990		

Trp Gly Val Val Phe Val Glu Ala Ile Leu Phe Phe Ala Gly Cys Glu
 995 1000 1005

Ala Trp Lys Trp Cys Lys Arg Ile Tyr Phe Arg His Thr Ser Gln
 1010 1015 1020

Lys Glu Thr Gly Arg Glu Arg Val Leu Arg Asp Phe Ser Arg Tyr
 1025 1030 1035

Thr Thr Met Ser Arg Ser Glu Thr Gln Ala Thr Gly Asp Leu Asn
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Val Glu Lys Ser Met Val
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<210> 196

<211> 2059

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Homologue GmZnf1; Phylum CEA284.2;

contig 4899 region 477626-479684

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 196

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gctacctatt	caggcgctca	agaatgccga	tgcctgaatt	cgcagttgac	tggcaagttt	240
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ttgtcatggg	cgtgaagggtg	gattagagtc	tggttggtgc	tgaagatgta	taggagaaaa	480
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tctcagaatt	ggcatctcat	cacagagtcc	gtgtaattat	cacattagca	aaagccacaa	600
tgtcccaccc	cgatctatcg	accattctcg	aggtctaccc	cgaatgcgaa	gtcacctgct	660
acgggtacgc	tcccagccaa	cggcgccgct	gcagaatgcg	aaccaggaaa	gacaaccgag	720
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gcaccgcgaa cctggagct 2059

<210> 197

<211> 1059

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Homologue GmZnf1; Phylum CEA284.2;

contig 4899 region 477626-479684

Genomic sequence containing the coding region

<400> 197

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gccccgctag	ttctctgcac	acgcttccac	caataccagg	cagacgactt	ggtccgggac	360
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gacgatgacg	accttgtata	ttgcaaaaac	cagtgcggta	cgaactatca	caaagcctgt	960
attgacgtgt	ggcatgctac	tcagcgtaca	tttgaaactc	cacgtgggga	tcctatcggc	1020
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<210> 198

<211> 1059

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Homologue GmZnf1; Phylum CEA284.2;

contig 4899 region 477626-479684

Coding region without introns

<400> 198

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accattctcg	aggtctaccc	cgaatgcgaa	gtcacctgct	acgggtacgc	tcccagccaa	180
cggcgccgct	gcagaatgcg	aaccaggaaa	gacaaccgag	acagggcttc	gtaccttctc	240
gaagagggca	ccagatatct	tcagcgcggc	ctccccgctc	acgggtctgct	tattgagcta	300
gccccgctag	ttctctgcac	acgcttccac	caataccagg	cagacgactt	ggtccgggac	360
tggcggggca	agctgcggga	gttccagcag	cagactcttc	tgaatgctat	gctgaaatcg	420
ctccaagagc	ttgtggacag	tcgggcgcgt	tcgcgtgctg	ctaggtcggc	gggtcggcgt	480
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gagcctgaac	cagaacccga	acctgaacct	gaacttacct	ccagccggtc	atctacggag	660
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agaagagtca	ctcgcaaac	aatcgaagga	gactgtacta	tctgcctgtg	tcctctacga	780
gaacaagaca	gtgatgaaaa	cggcgaggga	tcagaagatc	gcgatgatga	gaatgaggat	840
gatgcggcgg	gcacagggtc	cggcacagcg	tccgacgagc	acgacgcccc	cgaagaacat	900

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gacgatgacg accttggtata ttgcaaaaac cagtgcggtg cgaactatca caaagcctgt    960
attgacgtgt ggcattgctac tcagcgtaca tttgaaactc cacgtgggga tcctatcggc    1020
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<210> 199

<211> 352

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Homologue GmZnf1; Phylum CEA284.2;
 contig 4899 region 477626-479684
 Protein sequence

<400> 199

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Leu Ala Ser His His Arg Val Arg Val Ile Ile Thr Leu Ala Lys Ala
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Thr Met Ser His Pro Asp Leu Ser Thr Ile Leu Glu Val Tyr Pro Glu
          35              40              45

Cys Glu Val Thr Cys Tyr Gly Tyr Ala Pro Ser Gln Arg Arg Arg Cys
          50              55              60

Arg Met Arg Thr Arg Lys Asp Asn Arg Asp Arg Ala Ser Tyr Leu Leu
65              70              75              80

Glu Glu Gly Thr Arg Tyr Leu Gln Arg Gly Leu Pro Val Asp Gly Leu
          85              90              95

Leu Ile Glu Leu Ala Pro Leu Val Leu Cys Thr Arg Phe His Gln Tyr
          100             105             110

Gln Ala Asp Asp Leu Val Arg Asp Trp Arg Ala Lys Leu Arg Glu Phe
          115             120             125

Gln Gln Gln Thr Leu Leu Asn Ala Met Leu Lys Ser Leu Gln Glu Leu
          130             135             140

Val Asp Ser Arg Ala Arg Ser Arg Ala Ala Arg Ser Ala Gly Arg Arg
145             150             155             160

Leu Pro Glu Arg Val Ser Ser Pro Thr Arg Leu Glu Arg Ser Ala Ala
          165             170             175

Ile Val Thr Glu Glu Glu Pro Ala Ala Pro Glu Arg Glu Glu Glu Glu
          180             185             190

Glu Glu Arg Gly Asp Arg Glu Asp Glu Pro Glu Pro Glu Pro Glu Pro
          195             200             205

Glu Pro Glu Leu Thr Pro Ser Arg Ser Ser Thr Glu Thr Ser Ser Pro
          210             215             220

Ala Val Glu Ala His Val Ala Glu Pro Thr Val Pro Gln Thr Glu Ser
225             230             235             240

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Arg Arg Val Thr Arg Lys Pro Ile Glu Gly Asp Cys Thr Ile Cys Leu
 245 250 255
 Cys Pro Leu Arg Glu Gln Asp Ser Asp Glu Asn Gly Glu Gly Ser Glu
 260 265 270
 Asp Arg Asp Asp Glu Asn Glu Asp Asp Ala Ala Gly Thr Gly Ser Gly
 275 280 285
 Thr Ala Ser Asp Glu His Asp Ala Pro Glu Glu His Asp Asp Asp Asp
 290 295 300
 Leu Val Tyr Cys Lys Asn Gln Cys Gly Thr Asn Tyr His Lys Ala Cys
 305 310 315 320
 Ile Asp Val Trp His Ala Thr Gln Arg Thr Phe Glu Thr Pro Arg Gly
 325 330 335
 Asp Pro Ile Gly Leu Ser Cys Pro Tyr Cys Arg Ala Ala Trp Ser Ser
 340 345 350